STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 163666

TO: John Ulm
Location: rem/4E79/4C70
Art Unit: 1649
Sept. 1, 2005

Case Serial Number: 10/719692

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

STIC-Biotech/ChemLib 163 666 MG

From: Ulm, John
Sent: Wednesday, August 24, 2005 9:58 AM
To: STIC-Biotech/ChemLib
Subject: search SEQ ID NO:6 of application Serial Number 10/719,692

Please search SEQ ID NO:6 of application Serial Number 10/719,692.
John Ulm. 571 272-0880, Room REM 4E79, mail box REM 4C70, results prefered in paper.

Thank you.

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed:_____
Searcher Prep/Rev. Time:___
Online Time:_____

****
Type of Search

NA#:_____ AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

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OM protein - protein search, using sw model

Run on: August 30, 2005, 18:20:50 ; Search time 166 Seconds
(without alignments)
806.139 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1853	100.0	346	4	AAG80968	Aag80968 Human nGP
2	1853	100.0	346	4	ABB44522	Abb44522 Human GPC
3	1853	100.0	346	4	AAU06197	Aau06197 Novel hum
4	1853	100.0	346	4	AAU04373	Aau04373 Human G-p
5	1853	100.0	346	5	AAE16172	Aae16172 Human G-p
6	1853	100.0	346	5	AAU11401	Aau11401 HM74-like
7	1853	100.0	346	5	AAE17077	Aae17077 Human G-p
8	1853	100.0	346	5	ABB08596	Abb08596 Human lip
9	1853	100.0	346	5	ABG93786	Abg93786 Human G p
10	1853	100.0	346	5	ABP95599	Abp95599 Human GPC
11	1853	100.0	346	5	AAO14788	Aao14788 Human pur
12	1853	100.0	346	5	AAE24354	Aae24354 Human G p
13	1853	100.0	346	6	ABP81747	Abp81747 Human che
14	1853	100.0	346	6	ABP56751	Abp56751 Human GAV
15	1853	100.0	346	6	AAO26511	Aao26511 Human G-P
16	1853	100.0	346	6	ABP58453	Abp58453 Human res
17	1853	100.0	346	7	ADC46872	Adc46872 Human TA-
18	1853	100.0	346	7	ABW00810	Abw00810 Human GPC
19	1853	100.0	346	7	ADE40282	Ade40282 Human NOV
20	1853	100.0	346	7	ADE40272	Ade40272 Human NOV
21	1853	100.0	346	7	ADE40278	Ade40278 Human NOV
22	1853	100.0	346	7	ABW02123	Abw02123 Human GPC
23	1853	100.0	346	7	ADI21235	Adi21235 Novel hum
24	1853	100.0	346	7	ADL96470	Adl96470 Human G p
25	1853	100.0	346	8	ADJ71681	Adj71681 Human NOV
26	1853	100.0	346	8	ADJ71689	Adj71689 Human NOV
27	1853	100.0	346	8	ADJ71677	Adj71677 Human NOV
28	1853	100.0	346	8	ADM46116	Adm46116 Human 5-o
29	1853	100.0	346	8	ADO29444	Ado29444 Human GPC
30	1853	100.0	346	8	ADT08049	Adt08049 Human che
31	1853	100.0	352	7	ADE40286	Ade40286 Human NOV
32	1853	100.0	584	7	ADF70465	Adf70465 Orphan re
33	1849	99.8	346	6	ABB82502	Abb82502 Human TGR
34	1848	99.7	345	8	ADJ71693	Adj71693 Human NOV
35	1846	99.6	346	7	ADE40274	Ade40274 Human NOV
36	1846	99.6	346	8	ADJ71683	Adj71683 Human NOV
37	1839	99.2	346	4	ABB44523	Abb44523 Human GPC
38	1839	99.2	346	7	ADE40276	Ade40276 Human NOV
39	1839	99.2	346	7	ABW02124	Abw02124 Human GPC
40	1839	99.2	346	8	ADJ71685	Adj71685 Human NOV
41	1739	93.8	342	5	ABP54312	Abp54312 Human G p
42	1686	91.0	314	7	ADE40280	Ade40280 Human NOV
43	1686	91.0	314	8	ADJ71687	Adj71687 Human NOV
44	1686	91.0	320	7	ADE40288	Ade40288 Human NOV
45	1686	91.0	320	7	ADE40284	Ade40284 Human NOV

ALIGNMENTS

RESULT 1
AAG80968
ID AAG80968 standard; protein; 346 AA.
XX
AC AAG80968;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human nGPCR11 #2.
XX
KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder/attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200136473-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000WO-US031581.
XX
PR 16-NOV-1999; 99US-0165838P.
PR 17-NOV-1999; 99US-0166071P.
PR 19-NOV-1999; 99US-0166678P.
PR 28-DEC-1999; 99US-0173396P.
PR 22-FEB-2000; 2000US-0184129P.
PR 28-FEB-2000; 2000US-0185421P.
PR 28-FEB-2000; 2000US-0185554P.
PR 02-MAR-2000; 2000US-0186530P.
PR 03-MAR-2000; 2000US-0186811P.
PR 09-MAR-2000; 2000US-0188114P.
PR 17-MAR-2000; 2000US-0190310P.
PR 21-MAR-2000; 2000US-0190800P.
PR 20-APR-2000; 2000US-0198568P.
PR 02-MAY-2000; 2000US-0201190P.
PR 08-MAY-2000; 2000US-0203111P.
PR 25-MAY-2000; 2000US-0207094P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;

PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX
DR WPI; 2001-389826/41.
DR N-PSDB; AAH51008.
XX
PT New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
PT useful for diagnosing and treating e.g. schizophrenia.
XX
PS Claim 37; Page 89; 261pp; English.
XX
CC The present invention relates to novel G protein-coupled receptors
CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC one such G protein-coupled receptor. GPCRs are also known as seven
CC transmembrane receptors and function in signal transduction. The nGPCRx
CC coding sequences are useful for screening a human to diagnose a disorder
CC affecting the brain or a genetic predisposition, specifically
CC schizophrenia. nGPCRx are useful for identifying compounds useful for
CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC metabolic and cardiovascular diseases, proliferative disorders and
CC hormonal disorders. Modulators of nGPCRx activity have the utility for
CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

RESULT 2
ABB44522
ID ABB44522 standard; protein; 346 AA.
XX
AC ABB44522;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human GPCR1a polypeptide SEQ ID NO 2.
XX
KW Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
KW anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity;
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW infection; human immunodeficiency virus; HIV.
XX
OS Homo sapiens.
XX
PN WO200174904-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US010241.
XX
PR 31-MAR-2000; 2000US-0193664P.
PR 05-APR-2000; 2000US-0194614P.
PR 06-APR-2000; 2000US-0195063P.
PR 06-APR-2000; 2000US-0195066P.
PR 06-APR-2000; 2000US-0195067P.
PR 06-APR-2000; 2000US-0195068P.
PR 06-APR-2000; 2000US-0195069P.
PR 06-APR-2000; 2000US-0195070P.
PR 06-APR-2000; 2000US-0195510P.
PR 21-JUL-2000; 2000US-0219855P.
PR 27-JUL-2000; 2000US-0221284P.
PR 28-JUL-2000; 2000US-0221325P.
PR 11-AUG-2000; 2000US-0224588P.
PR 11-OCT-2000; 2000US-0239613P.
PR 18-JAN-2001; 2001US-0262508P.
PR 23-JAN-2001; 2001US-0263433P.
PR 23-JAN-2001; 2001US-0263604P.
PR 30-JAN-2001; 2001US-0265161P.
PR 29-MAR-2001; 2001US-00823172.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
PI Padigaru M, Mishnu VS, Tchernev VT, Spytek KA, Li L, Baumgartner JC;
PI Gusev VY;
XX
DR WPI; 2001-639351/73.
DR N-PSDB; ABA81529, ABA81530.
XX
PT New human G-protein coupled receptor X, GPCRX, polypeptide useful in
PT treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy
PT or atherosclerosis, and to screen for antagonists and agonists useful
PT therapeutically.
XX
PS Claim 1; Page 8; 157pp; English.
XX
CC The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
CC encode G-coupled protein-receptor related polypeptides (ABB44522-
CC ABB44543). The isolated polypeptide having a sequence differing by no
CC more than 15 % of amino acid residues from one of 22 amino acid sequences
CC (or mature forms of the sequences), fully defined in the specification
CC and corresponding to human G-protein coupled receptor X (GPCRX)
CC polypeptides. The polypeptides have potential cardiant,
CC antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
CC polypeptides can be administered therapeutically, especially using gene
CC therapy and expressing the encoding DNA in vivo, to treat or prevent
CC GPCRX-associated disorders, especially in humans. For example, they can
CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
CC related to signal processing and metabolic pathway modulation (e.g.
CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
CC haematopoietic disorders, developmental diseases, neurological disorders,
CC bacterial, fungal, protozoal and viral infections (e.g. with human
CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
CC to determine the presence of or predisposition to a disease associated
CC with altered levels of the polypeptide in mammals (especially humans) by
CC detecting alterations in polypeptide expression levels relative to
CC control samples. They are useful to identify agents binding polypeptide
CC (e.g. cellular receptors or downstream effectors) and/or agents

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CC   modulating cellular polypeptide expression or activity, useful as
CC   antagonists and agonists in disease treatment
XX
SQ   Sequence 346 AA;

  Query Match           100.0%;  Score 1853;  DB 4;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 3
AAU06197
ID   AAU06197 standard; protein; 346 AA.
XX
AC   AAU06197;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Novel human G protein-coupled receptor (GPCR) protein.
XX
KW   Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
KW   hyperproliferative disorder; neurological disorder; psychiatric disease;
KW   inflammatory disorder; respiratory disorder.
XX
OS   Homo sapiens.
XX
PN   WO200173029-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009522.
XX
PR   27-MAR-2000; 2000US-0192419P.
PR   06-SEP-2000; 2000US-0230459P.
PR   20-SEP-2000; 2000US-00666535.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Ye J,  Cravchik A,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2001-616503/71.
DR   N-PSDB; AAS12581.
XX
PT   Novel human G-protein coupled receptor proteins and nucleic acid
PT   molecules encoding the protein for use in developing human therapeutics
PT   and diagnostic compositions and for identifying modulators of the
PT   protein.
XX
PS   Claim 1; Fig 1; 66pp; English.
XX
CC   The present invention relates to the isolation of a novel human G-protein
CC   coupled receptor (GPCR) which is related to the chemokine receptor
CC   subfamily. The cDNA and gene sequences encoding for GPCR are also given
CC   in the invention. The sequences of the invention are useful for
CC   diagnosing and treating diseases or conditions mediated by human
CC   proteases. Such diseases include hyperproliferative disorders (e.g.
CC   hyperplasia), neurological disorders (e.g. Parkinson's disease),
CC   psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g.
CC   diabetes) and respiratory disorders (e.g. adult respiratory distress
CC   syndrome, ARDS). The GPCR protein is also useful for identifying a
CC   modulator of the expression of the protein. It also serves as a target
CC   for identifying agents for use in mammalian therapeutic applications,
CC   e.g. a human drug, particularly modulating a biological or pathological
CC   response in a cell or tissue that expresses the protein, in biological
CC   assays related to GPCRs that are related to members of the chemokine
CC   receptor subfamily, in drug screening assays and in competition binding
CC   assays. GPCR is also useful in diagnosing a disease or predisposition to
CC   a disease mediated by the peptide, in pharmacogenomic analysis. The
CC   polynucleotide sequences can also be used in gene therapy. The present
CC   sequence represents the novel human GPCR of the invention
XX
SQ   Sequence 346 AA;

  Query Match           100.0%;  Score 1853;  DB 4;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 4
AAU04373
ID   AAU04373 standard; protein; 346 AA.
XX
AC   AAU04373;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human G-protein coupled receptor, hRUP19.
XX
KW   Human; G-protein coupled receptor; GPCR; hRUP19; agonist;
KW   inverse agonist; lung cancer.
XX
OS   Homo sapiens.
XX
PN   WO200136471-A2.
XX
PD   25-MAY-2001.
XX
PF   16-NOV-2000; 2000WO-US031509.
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XX
PR   17-NOV-1999;   99US-0166088P.
PR   17-NOV-1999;   99US-0166099P.
PR   17-NOV-1999;   99US-0166369P.
PR   23-DEC-1999;   99US-0171900P.
PR   23-DEC-1999;   99US-0171901P.
PR   23-DEC-1999;   99US-0171902P.
PR   11-FEB-2000; 2000US-0181749P.
PR   14-MAR-2000; 2000US-0189258P.
PR   14-MAR-2000; 2000US-0189259P.
PR   10-APR-2000; 2000US-0195898P.
PR   10-APR-2000; 2000US-0195899P.
PR   10-APR-2000; 2000US-0196078P.
PR   28-APR-2000; 2000US-0200419P.
PR   12-MAY-2000; 2000US-0203630P.
PR   12-JUN-2000; 2000US-0210741P.
PR   12-JUN-2000; 2000US-0210982P.
PR   21-AUG-2000; 2000US-0226760P.
PR   26-SEP-2000; 2000US-0235418P.
PR   26-SEP-2000; 2000US-0235779P.
PR   20-OCT-2000; 2000US-0242332P.
PR   20-OCT-2000; 2000US-0242343P.
PR   24-OCT-2000; 2000US-0243019P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Chen R,  Dang HT,  Lowitz KP;
XX
DR   WPI; 2001-355616/37.
DR   N-PSDB; AAS07946.
XX
PT   Endogenous and non-endogenous versions of human G-protein coupled
PT   receptors for direct identification of candidate compounds as agonists,
PT   inverse agonists or partial agonists for use as therapeutic agents.
XX
PS   Claim 45; Page 110-111; 160pp; English.
XX
CC   The sequence represents a human G-protein coupled receptor (GPCR),
CC   hRUP19. The endogenous and non-endogenous, constitutively activated
CC   versions of human G-protein coupled receptors (GPCR), are useful for
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists having applicability as therapeutic
CC   agents for treating diseases related to GPCR, e.g. lung cancer. Non-
CC   endogenous version of human GPCRs are also utilized in research settings
CC   and in vitro and in vivo system, incorporating GPCRs can be utilised to
CC   elucidate and understand the roles these receptors play in the human
CC   condition, both normal and diseased
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 4;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 5
AAE16172
ID   AAE16172 standard; protein; 346 AA.
XX
AC   AAE16172;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor 3 (GCREC-3) protein.
XX
KW   Human; G-protein coupled receptor 3; cell proliferative disorder;
KW   arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
KW   Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW   atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
KW   gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
KW   acquired immune deficiency syndrome; inflammatory disorder; infection;
KW   Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
KW   diabetes; obesity; osteoporosis; gene therapy; GCREC-3.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .32
FT                   /label= Signal_peptide
FT   Domain          20. .44
FT                   /note= "Transmembrane domain"
FT   Protein         33. .346
FT                   /label= Human_mature_GCREC-3_protein
FT   Domain          93. .110
FT                   /note= "Transmembrane domain"
FT   Domain          137. .154
FT                   /note= "Transmembrane domain"
FT   Domain          222. .244
FT                   /note= "Transmembrane domain"
XX
PN   WO200187937-A2.
XX
PD   22-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016285.
XX
PR   18-MAY-2000; 2000US-0205628P.
PR   22-MAY-2000; 2000US-0206222P.
PR   25-MAY-2000; 2000US-0207566P.
PR   02-JUN-2000; 2000US-0208834P.
PR   02-JUN-2000; 2000US-0208861P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Patterson C,  Lu DAM,  Thornton M,  Lu Y,  Tribouley CM,  Graul R;
PI   Khan FA,  Gandhi AR,  Walia NK,  Nguyen DB,  Yue H,  Hafalia A;
PI   Elliott VS,  Lal P,  Reddy R,  Kallick DA,  Tang TY,  Au-Young J;
XX
DR   WPI; 2002-089844/12.
DR   N-PSDB; AAD26371.
XX
PT   Novel G-protein coupled receptors and polynucleotides useful for
PT   diagnosis, treatment and prevention of disorders of cell proliferation,
PT   neurological, cardiovascular, metabolic disorders and viral infections.
XX
PS   Claim 1; Page 105-106; 115pp; English.
XX
CC   The invention relates to human G-protein coupled receptor (GCREC)
CC   polypeptides and polynucleotides. GCREC polypeptides are useful for
CC   screening compounds that modulate their activity. They are useful in the
CC   diagnosis, prevention and treatment of disorders which include cell
CC   proliferative disorders such as arteriosclerosis, hepatitis,
```

```
CC   myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
CC   lymphoma; neurological disorders such as epilepsy, ischaemic
CC   cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
CC   Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
CC   meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
CC   cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
CC   hypertension, vascular tumours, myocardial infarction, hypertensive heart
CC   disease, infective endocarditis, cardiomyopathy, myocarditis;
CC   gastrointestinal disorders such as dysphagia, peptic oesophagitis,
CC   emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
CC   constipation, acquired immune deficiency syndrome (AIDS), hepatic
CC   encephalopathy; autoimmune/inflammatory disorders such as Addison's
CC   disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
CC   dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
CC   emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
CC   arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
CC   fungal, parasitic, protozoal and helminthic infections and trauma;
CC   metabolic disorders such as diabetes, obesity and osteoporosis; and viral
CC   infections such as infection caused by viral agent classified as
CC   adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are
CC   useful as probes for assessing toxicity of test compounds. They are also
CC   used in gene therapy. The present sequence is human G-protein coupled
CC   receptor 3 (GCREC-3) protein
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 6
AAU11401
ID   AAU11401 standard; protein; 346 AA.
XX
AC   AAU11401;
XX
DT   26-FEB-2002  (first entry)
XX
DE   HM74-like G-protein coupled receptor (GPCR).
XX
KW   HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide;
KW   protozoacide; analgesic; cytostatic; neuroleptic; nootropic;
KW   anticonvulsant; tranquilliser; viral infection; pain; cancer; anorexia;
KW   bulimia; asthma; central nervous system disease; CNS disease;
KW   cardiovascular disease; hypotension; hypertension; angina pectoris;
KW   myocardial infarction; urinary retention; osteoporosis; ulcer; asthma;
KW   inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis;
KW   psychotic disorder; neurological disorder; dyskinesia;
KW   Huntington's disease; Tourette's syndrome; anxiety; schizophrenia;
KW   manic depression; delirium; dementia; mental retardation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          20. .37
FT                   /label= Transmembrane_domain_1
FT   Domain          53. .73
FT                   /label= Transmembrane_domain_2
FT   Domain          91. .113
FT                   /label= Transmembrane_domain_3
FT   Region          101. .118
FT                   /label= GPCR_region
FT                   /note= "G-protein coupled receptor region"
FT   Domain          133. .150
FT                   /label= Transmembrane_domain_4
FT   Domain          180. .197
FT                   /label= Transmembrane_domain_5
FT   Domain          223. .242
FT                   /label= Transmembrane_domain_6
FT   Domain          260. .279
FT                   /label= Transmembrane_domain_7
XX
PN   WO200177320-A2.
XX
PD   18-OCT-2001.
XX
PF   04-APR-2001; 2001WO-EP003811.
XX
PR   05-APR-2000; 2000US-0194701P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2002-049147/06.
DR   N-PSDB; AAS18501.
XX
PT   Novel isolated polynucleotide, useful for treating infection, pain,
PT   cancer, asthma, hypertension, myocardial infarction, urinary retention,
PT   osteoporosis, encodes the human HM74-like G-protein coupled receptor
PT   polypeptide.
XX
PS   Claim 1; Fig 2; 77pp; English.
XX
CC   The invention describes a novel isolated polynucleotide (I) encoding a
CC   human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents
CC   that regulate HM74-like GPCR are useful for modulating the activity of
CC   the protein in a disease selected from bacterial, fungal, protozoan, and
CC   viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous
CC   system (CNS) disease, cardiovascular disease, hypotension, hypertension,
CC   angina pectoris, myocardial infarction, urinary retention, osteoporosis,
CC   ulcer, asthma, inflammation, allergy, benign prostatic hypertrophy,
CC   multiple sclerosis and dyskinesia such as Huntington's disease and
CC   Tourette's syndrome. The composition is also useful for treating
CC   psychotic and neurological disorders such as anxiety, schizophrenia,
CC   manic depression, delirium, dementia and severe mental retardation. (I)
CC   or the HM74-like GPCR polypeptide are also useful for treating the above
CC   mentioned diseases. (I) is useful in a diagnostic assay for detecting
CC   diseases, susceptibility to diseases and abnormalities related to the
CC   presence of mutations in the nucleic acid sequences which encode a GPCR.
CC   The polypeptide is useful to identify test compounds which may act as
CC   agonists or antagonists at the receptor site and which can be regulated
CC   to provide therapeutic effects. The polypeptide is also useful as a bait
CC   protein in a two-hybrid or three-hybrid assay, and to immunise a mammal
CC   for production of polyclonal antibodies. This the amino acid sequence of
CC   human HM74-like GPCR described in the method of the invention
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
```

```
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 7
AAE17077
ID   AAE17077 standard; protein; 346 AA.
XX
AC   AAE17077;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human G-protein coupled receptor (GPCRx14) protein.
XX
KW   Human; G-protein coupled receptor; GPCRx14; cerebroprotective; vomiting;
KW   receptor-mediated disorder; therapy; urinary retention; allergy; obesity;
KW   osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
KW   anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
KW   stroke; hypertension; neuronal disorder; myocardial infarction psychotic;
KW   depression; mental retardation; neurodegenerative disease; antibacterial;
KW   Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;
KW   Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KW   vulnerary; analgesic; anorectic; anabolic; diuretic; cardiant; nootropic;
KW   antiemetic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          17. .40
FT                   /note= "Transmembrane domain"
FT   Domain          52. .70
FT                   /note= "Transmembrane domain"
FT   Domain          90. .111
FT                   /note= "Transmembrane domain"
FT   Domain          132. .152
FT                   /note= "Transmembrane domain"
FT   Domain          185. .203
FT                   /note= "Transmembrane domain"
FT   Domain          221. .237
FT                   /note= "Transmembrane domain"
FT   Domain          258. .281
FT                   /note= "Transmembrane domain"
XX
PN   WO200198330-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-BE000104.
XX
PR   20-JUN-2000; 2000US-0212913P.
PR   11-JUL-2000; 2000US-0217494P.
PR   26-JAN-2001; 2001EP-00870015.
PR   12-FEB-2001; 2001EP-00870024.
XX
PA   (EURO-) EUROSCREEN SA.
XX
PI   Lannoy V,  Brezillon S,  Detheux M,  Parmentier M,  Govarts C;
XX
DR   WPI; 2002-130789/17.
DR   N-PSDB; AAD27497.
XX
PT   New G-protein coupled receptor, useful in the manufacture of medicaments
PT   for treating receptor mediated disorders e.g. acute heart failure and
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 29; 46pp; English.
XX
CC   The present invention relates to a G-protein coupled receptor (GPCR) and
CC   nucleotide encoding it. GPCR are useful in the manufacture of a
CC   medicament for the prevention and/or treatment of receptor-mediated
CC   disorders e.g. viral infections, virus and bacterial diseases, diseases
CC   and disorders involving disturbances of cell migration, diseases or
CC   perturbations of immune system including cancers, development of tumours
CC   and tumour metastasis, inflammatory and neoplastic processes; bacterial
CC   and fungal infections, in wound and bone healing, dysfunction of
CC   regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia,
CC   urinary retention, osteoporosis, angina pectoris, atherosclerosis,
CC   restenosis, diseases involving excessive or reduced proliferation or loss
CC   of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies,
CC   benign prostatic hypertrophy, migraine, vomiting; blood circulating
CC   affections including acute heart failure, hypotension, hypertension and
CC   myocardial infarction psychotic; neuronal disorders such as anxiety,
CC   schizophrenia, maniac depression, depression, delirium, dementia, severe
CC   mental retardation; degenerative diseases; neurodegenerative diseases
CC   such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g.
CC   Huntington's disease or Gilles de la Tourette's syndrome and other
CC   related diseases. The present sequence is GPCRx14 protein
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 8
ABB08596
ID   ABB08596 standard; protein; 346 AA.
XX
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```
AC   ABB08596;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human lipocyte-originated G protein-coupled receptor protein TGR13.
XX
KW   Antiinflammatory; anorectic; obesity; inflammation; gene therapy; human;
KW   G protein-coupled receptor protein TGR13.
XX
OS   Homo sapiens.
XX
PN   WO200202767-A1.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-JP005711.
XX
PR   04-JUL-2000; 2000JP-00206860.
PR   31-JUL-2000; 2000JP-00235274.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Shibata S,  Horikoshi K,  Taniyama Y,  Shintani Y,  Miyajima N;
XX
DR   WPI; 2002-164535/21.
DR   N-PSDB; ABA99236.
XX
PT   New human lipocyte-originated G protein-coupled receptor proteins TGR13
PT   and encoding DNAs, for developing drugs to treat obesity and
PT   inflammations, including gene therapy.
XX
PS   Claim 1; Fig 2; 101pp; Japanese.
XX
CC   This invention relates to a human lipocyte-originated G protein-coupled
CC   receptor proteins TGR13, thought to be antiinflammatory and anorectic in
CC   their action. The proteins and encoded DNAs are for use in developing
CC   drugs to treat obesity and inflammation, including gene therapy. The
CC   present sequence represents the human lipocyte-originated G protein-
CC   coupled receptor protein TGR13
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 9
ABG93786
ID   ABG93786 standard; protein; 346 AA.
XX
AC   ABG93786;
XX
DT   26-NOV-2002  (first entry)
XX
DE   Human G protein-coupled receptor protein, nGPCR-11.
XX
KW   Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW   nG protein coupled receptor; communication; serpentine structure;
KW   seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW   genetic predisposition; brain; immune response; gene therapy;
KW   anxiety disorder; depression; bipolar disorder; schizophrenia;
KW   Huntington's disease; dyskinesia; manic depression; stroke;
KW   Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   WO200264789-A1.
XX
PD   22-AUG-2002.
XX
PF   14-FEB-2001; 2001WO-US004641.
XX
PR   14-FEB-2001; 2001WO-US004641.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Lind P,  Parodi LA,  Vogeli G,  Wood LS;
XX
DR   WPI; 2002-674879/72.
DR   N-PSDB; ABS70241.
XX
PT   New nucleic acids and polypeptides of the nG protein-coupled receptor,
PT   useful for treating or diagnosing a mental disorder or a disorder
PT   affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
PT   Parkinson's disease.
XX
PS   Example 1; Page 84; 244pp; English.
XX
CC   The invention discloses an isolated human polypeptide, and encoding
CC   nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC   nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
CC   communication between cells and their environment and are characterised
CC   by a serpentine structure that passes through the cell membrane seven
CC   times, hence the reason such receptors are sometimes called seven
CC   transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC   useful for identifying an nGPCR allelic variant that correlates with a
CC   mental disorder, for isolating an antibody that binds to an epitope of
CC   the polypeptide, for identifying a compound that binds the polypeptide or
CC   polynucleotide and/or modulates its biological activity, for screening a
CC   human subject to diagnose a disorder, or a genetic predisposition to a
CC   disorder, affecting the brain or a genetic disposition to the disorder,
CC   for identifying compounds useful for the treatment of a mental disorder
CC   and for identifying a compound useful as a modulator of binding between
CC   nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
CC   useful for inducing an immune response in a mammal. The nucleic acid or
CC   polypeptide is particularly useful, using gene therapy, for treating e.g.
CC   anxiety disorders, depression, bipolar disorder, schizophrenia,
CC   Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
CC   disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC   be used for treating diabetes, inflammation or wounds. The sequences
CC   presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
CC   referred to as beGPCRs) proteins
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
```

```
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

RESULT 10
ABP95599
ID ABP95599 standard; protein; 346 AA.
XX
AC ABP95599;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polypeptide SEQ ID NO 8.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB001446.
XX
PR 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
DR N-PSDB; ABZ42873.
XX
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 10; SEQ ID NO 8; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

RESULT 11
AAO14788
ID AAO14788 standard; protein; 346 AA.
XX
AC AAO14788;
XX
DT 28-JUN-2002 (first entry)
XX
DE Human purinergic-like G-protein coupled receptor (AXOR87).
XX
KW Human; purinergic-like G-protein coupled receptor; AXOR87; immunity;
KW autoimmunity; inflammation; immunodeficiency; bacterial infection;
KW fungal infection; viral infection; protozoa infection; cancer; diabetes;
KW obesity; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;
KW osteoarthritis; psychotic disorder; neurological disorder; vaccine;
KW chromosome 12q24.
XX
OS Homo sapiens.
XX
PN GB2365868-A.
XX
PD 27-FEB-2002.
XX
PF 25-MAY-2001; 2001GB-00012860.
XX
PR 30-MAY-2000; 2000US-00580675.
PR 02-NOV-2000; 2000GB-00026839.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Ignar DM, Elshourbagy N, Gattu M, Shabon U;
XX
DR WPI; 2002-364852/40.
DR N-PSDB; AAL42499.
XX
PT New purinergic-like G-protein coupled receptor AXOR87 polypeptide and
PT polynucleotide, useful for treating diseases related to autoimmunity,
PT inflammation, immunodeficiency, or bacterial, fungal, viral and protozoal
PT infections.

```
XX
PS   Claim 2; Page 36; 47pp; English.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   purinergic-like G-protein coupled receptor AXOR87. The AXOR87 DNA and
CC   protein sequences of the invention may be used for treating diseases
CC   related to immunity, autoimmunity, inflammation, immunodeficiency, and
CC   infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and
CC   protein sequences are particularly useful for treating: cancers,
CC   diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid
CC   arthritis, osteoarthritis, as well as psychotic and neurological
CC   disorders. The AXOR87 DNA and protein sequences may also be used as
CC   vaccines. The present amino acid sequence (encoded by a sequence located
CC   on chromosome 12q24) represents the human AXOR87 protein
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 12
AAE24354
ID   AAE24354 standard; protein; 346 AA.
XX
AC   AAE24354;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Human G protein coupled receptor (GPCR), 57242 protein.
XX
KW   Human; G protein coupled receptor; GPCR; 57242 protein; overweight;
KW   metabolic disorder; lipogenesis; lipolysis; immunomodulator; heart;
KW   bone disorder; osteoporosis; osteogenesis; bone resorption; cachexia;
KW   hyperlipidaemia; anorexia; haematopoietic disorder; osteopathic;
KW   autoimmune disorder; psoriasis; multiple sclerosis; brain disorder;
KW   degenerative disease; Alzheimer's disease; Pick disease; diabetes;
KW   adipocyte; hyperplastic growth; hypertrophic growth; gene therapy;
KW   obesity; anorectic; receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .37
FT                   /label= Signal_peptide
FT   Domain          1. .20
FT                   /note= "N-terminal non-transmembrane domain"
FT   Modified-site   3. .6
FT                   /note= "N-glycosylation site"
FT   Cleavage-site   9. .10
FT                   /note= "Cleavage site for mitochondrial preseq"
FT   Domain          21. .42
FT                   /note= "Transmembrane domain"
FT   Domain          32. .278
FT                   /note= "GPCR domain"
FT   Protein         38. .346
FT                   /note= "Human mature GPCR protein"
FT   Domain          43. .51
FT                   /note= "Non-transmembrane domain"
FT   Domain          52. .70
FT                   /note= "Transmembrane domain"
FT   Region          71. .89
FT                   /note= "Extracellular loop"
FT   Peptide         77. .80
FT                   /note= "Nuclear localisation signal"
FT   Domain          90. .111
FT                   /note= "Transmembrane domain"
FT   Domain          112. .130
FT                   /note= "Non-transmembrane domain"
FT   Domain          131. .152
FT                   /note= "Transmembrane domain"
FT   Region          153. .184
FT                   /note= "Extracellular loop"
FT   Domain          185. .201
FT                   /note= "Transmembrane domain"
FT   Domain          202. .220
FT                   /note= "Non-transmembrane domain"
FT   Peptide         204. .220
FT                   /note= "Nuclear localisation signal"
FT   Modified-site   216. .219
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Domain          221. .245
FT                   /note= "Transmembrane domain"
FT   Region          245. .258
FT                   /note= "Extracellular loop"
FT   Domain          246. .255
FT                   /note= "Non-transmembrane domain"
FT   Domain          259. .280
FT                   /note= "Transmembrane domain"
FT   Domain          281. .346
FT                   /note= "C-terminal cytoplasmic domain"
XX
PN   WO200218579-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US026882.
XX
PR   29-AUG-2000; 2000US-0228409P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Glucksmann MA;
XX
DR   WPI; 2002-479433/51.
DR   N-PSDB; AAD39181.
XX
PT   Human G protein coupled receptor nucleic acid and polypeptide molecules,
PT   designated 57242, useful for diagnosing, preventing or treating aberrant
PT   lipogenesis or aberrant lipolysis, obesity, diabetes or bone disorders
PT   (e.g. osteoporosis).
XX
PS   Claim 9; Page 112-113; 114pp; English.
XX
CC   The invention relates to G protein coupled receptor (GPCR) family member,
CC   57242 and its corresponding nucleic acid sequence. The 57242 nucleic acid
CC   and polypeptide are useful for diagnosing, preventing or treating a
CC   subject having or at risk of developing a metabolic disorder,
CC   particularly a disorder associated with aberrant lipogenesis or aberrant
CC   lipolysis, obesity or diabetes. The 57242 DNA and protein are also useful
```

```
CC   for treating a subject having bone disorder, where the disorder is
CC   osteoporosis or a disorder associated with aberrant osteogenesis or
CC   aberrant bone resorption. These diseases include obesity, diabetes,
CC   hyperlipidaemia, overweight, anorexia or cachexia. The 57242 DNA and
CC   protein are also useful for treating a subject having haematopoietic
CC   disorders, autoimmune disorders e.g. psoriasis and multiple sclerosis,
CC   brain disorders, degenerative diseases e.g. Alzheimer's disease and Pick
CC   disease and disorders involving heart. The 57242 nucleic acid and
CC   polypeptide are also useful for modulating adipocyte activity such as
CC   hyperplastic growth, hypertrophic growth or lipogenesis. The 57242 DNA is
CC   used in gene therapy. The present sequence is human 57242 protein
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 13
ABP81747
ID   ABP81747 standard; protein; 346 AA.
XX
AC   ABP81747;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human chemokine receptor FKSG80/GPR81 protein SEQ ID NO:668.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   N-PSDB; ABZ42592.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 346 AA;

  Query Match             100.0%;  Score 1853;  DB 6;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

```
RESULT 14
ABP56751
ID   ABP56751 standard; protein; 346 AA.
XX
AC   ABP56751;
XX
DT   31-MAR-2003  (first entry)
XX
DE   Human GAVE3 protein SEQ ID NO:2.
XX
KW   Human; GAVE3; G protein-coupled receptor; GPCR; antiinflammatory;
KW   antiasthmatic; antirheumatic; antiarthritic; inflammatory disorder;
KW   asthma; chronic obstructive pulmonary disease; rheumatoid arthritis;
KW   chromosome 12.
XX
OS   Homo sapiens.
XX
PN   WO2003000846-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-US019490.
XX
PR   22-JUN-2001; 2001US-00886041.
XX
PA   (AVET ) AVENTIS PHARM INC.
XX
PI   Xia T,  Ni D,  Eishingdrelo H,  Ardati A,  Minnich A,  Jupp R;
XX
DR   WPI; 2003-184040/18.
DR   N-PSDB; ABZ22648.
XX
PT   New GAVE3 nucleic acid and polypeptide, for preventing or treating a
PT   disorder associated with aberrant GAVE3 expression or activity, e.g.
PT   inflammatory disease, asthma, chronic obstructive pulmonary disease or
PT   rheumatoid arthritis.
XX
PS   Claim 9; Fig 2; 90pp; English.
XX
CC   The present sequence represents a human G protein-coupled receptor
CC   (GPCR), designated GAVE3. GAVE3 is located on human chromosome 12. GAVE3
CC   has antiinflammatory, antiasthmatic, antirheumatic and antiarthritic
CC   activities. GAVE3 nucleic acids, polypeptides, agonists and antagonists
CC   can be used for preventing or treating a disorder associated with
CC   aberrant GAVE3 expression or activity, e.g. inflammatory disorders such
CC   as asthma, chronic obstructive pulmonary disease or rheumatoid arthritis.
CC   The nucleic acids and polypeptides can also be useful for identifying
CC   modulators, i.e. candidate or test compounds, that bind to GAVE3 proteins
CC   or have a stimulatory or inhibitory effect on GAVE3 expression or
CC   activity. The nucleotide sequences can also be used for chromosomal
CC   mapping, tissue typing or forensic biology. Host cells comprising GAVE3
CC   can be used for producing non-human transgenic animals for studying the
CC   function and/or activity of GAVE3, or for identifying and/or evaluating
CC   modulators of GAVE3 activity
XX
SQ   Sequence 346 AA;

  Query Match            100.0%;  Score 1853;  DB 6;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 15
AAO26511
ID   AAO26511 standard; protein; 346 AA.
XX
AC   AAO26511;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human G-Protein Coupled Receptor protein.
XX
KW   Anorectic; antidiabetic; antilipaemic; antiasthmatic; antiinflammatory;
KW   antiallergic; antianginal; nephrotropic; hepatotropic; immunosuppressive;
KW   virucide; G-Protein-agonist; G-Protein-antagonist; dyslipidaemia; GPCR;
KW   G-Protein Coupled Receptor; obesity; diabetes; asthma; bronchitis;
KW   allergy; angina; glomerulonephritis; hepatitis; allograft rejection;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200283736-A2.
XX
PD   24-OCT-2002.
XX
PF   14-FEB-2002; 2002WO-US004397.
XX
PR   14-FEB-2001; 2001US-0269040P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Elliott SG,  Rogers N,  Busse LA;
XX
DR   WPI; 2003-075524/07.
DR   N-PSDB; AAL53846.
XX
PT   New GPCR polypeptide and encoding nucleic acid molecule, useful for
PT   diagnosis, treatment and/or prevention of diseases associated with GPCR
PT   polypeptides, such as obesity, diabetes, asthma, allergies, angina and
PT   hepatitis.
XX
PS   Claim 13; Fig 1; 122pp; English.
XX
CC   The invention relates to a novel isolated G-Protein Coupled Receptor
CC   (GPCR) protein. The methods and compositions of the present invention are
CC   useful for diagnosis, treatment, amelioration and/or prevention of
CC   diseases associated with G-Protein Coupled Receptor (GPCR) polypeptides,
CC   such as obesity, diabetes, dyslipidaemia, asthma, bronchitis, allergies,
CC   angina, glomerulonephritis, hepatitis and allograft rejection. This
CC   sequence represents the human GPCR protein of the invention
XX
SQ   Sequence 346 AA;

  Query Match            100.0%;  Score 1853;  DB 6;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-199;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
                ||||||||||||||||||||||||||||||||||||||||||||||
Db         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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Search completed: August 30, 2005, 18:30:49
Job time : 169 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:24:37 ; Search time 41 Seconds
(without alignments)
811.976 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	880.5	47.5	387	2	I69202	G protein-coupled
2	364	19.6	362	2	S33733	G protein-coupled
3	362.5	19.6	373	2	JC4162	P2Y receptor - bov
4	354	19.1	373	2	JC4737	G protein-coupled
5	343.5	18.5	370	2	JC5549	heptahelical P2Y5-
6	339	18.3	308	2	I50241	G protein-coupled
7	324	17.5	344	2	T09508	intron 17 purinerg
8	320	17.3	373	2	A47556	ATP receptor P2u -
9	310.5	16.8	420	2	I51667	thrombin receptor
10	309.5	16.7	363	2	I57940	somatostatin recep
11	307	16.6	391	2	C41795	somatostatin recep
12	305.5	16.5	391	2	A41795	somatostatin recep
13	305.5	16.5	391	2	A39297	somatostatin recep
14	304.5	16.4	359	2	S15403	angiotensin II rec
15	302.5	16.3	369	2	B41795	somatostatin recep
16	302	16.3	364	2	JQ1488	bradykinin B2 rece
17	302	16.3	399	2	I48705	proteinase activat
18	300.5	16.2	369	2	D41795	somatostatin recep
19	300.5	16.2	369	2	A45291	somatostatin recep
20	300	16.2	328	2	I55450	G protein-coupled
21	300	16.2	384	2	A47249	brain-specific som
22	300	16.2	428	2	A44021	somatostatin recep
23	299.5	16.2	369	2	JC2083	somatostatin recep
24	299	16.1	388	2	JN0605	somatostatin recep
25	298.5	16.1	418	2	A46226	somatostatin recep
26	298.5	16.1	432	2	A43448	thrombin receptor
27	298	16.1	428	2	S30508	probable G protein
28	297	16.0	397	2	S66518	proteinase-activat
29	296.5	16.0	346	2	S29248	somatostatin recep
30	296	16.0	359	2	A48857	angiotensin II rec
31	296	16.0	375	2	A54946	P-2U nucleotide re
32	295	15.9	384	2	JC4629	somatostatin recep
33	294	15.9	372	2	I38532	delta opioid recep
34	292.5	15.8	361	2	JC5653	G protein-coupled
35	292	15.8	371	2	JC5498	G protein-coupled
36	291.5	15.7	359	2	S44425	angiotensin II rec
37	291.5	15.7	359	2	JC2134	angiotensin II rec
38	290	15.7	372	2	S34592	delta opioid recep
39	289	15.6	359	2	JC1104	angiotensin II rec
40	288	15.5	355	2	A45177	chemokine (C-C) re
41	288	15.5	372	2	B48227	delta opioid recep
42	287.5	15.5	365	2	S68208	G protein-coupled
43	287.5	15.5	371	2	JC5796	probable chemoattr
44	286.5	15.5	359	2	JH0621	angiotensin II rec
45	286.5	15.5	423	2	JC7677	allatostatin recep

ALIGNMENTS

RESULT 1
I69202
G protein-coupled receptor HM74 - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I69202
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A;Reference number: I54751; MUID:94092629; PMID:7505609
A;Accession: I69202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867
C;Genetics:
A;Gene: HM74
C;Superfamily: G protein-coupled receptor 4

Query Match 47.5%; Score 880.5; DB 2; Length 387;
Best Local Similarity 52.2%; Pred. No. 3.2e-73;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

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Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||    | |::|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:|| | ||||||| || |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :  |     |  | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :||||||||| :|:||||:| |: | |::|:|  |||||||||: |:|||  |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  | ||||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              | |     |   : ::    ::      : : |   | |
Db        316 KMTGEPDNNRRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
```

RESULT 2
S33733
G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)

```
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstoc
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g3950
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             19.6%;  Score 364;  DB 2;  Length 362;
  Best Local Similarity   29.1%;  Pred. No. 9.5e-26;
  Matches   95;  Conservative   58;  Mismatches  130;  Indels   44;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |: | ||| ||:  | |||: |   :||:||||:|||| :: ||    ||
Db         43 LPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYYFN 102

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||: |::  |   :|  |||:||| ::  ||  ||||  ::  :  : | :
Db        103 KTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNAVYVSS 162

Qy        138 TLWALVIL---------GTVYLLLENHLCVQETA----------VSCESFIMESANGWHD 178
               :||||:          ||     :   |  ||           | :  |
Db        163 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM-------- 214

Qy        179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                 | :|  :|| |   || :|  :  |      :|:   :::|  ||   |||
Db        215 ------FCIPFIVILGCYGLIVKALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYLPFHV 267

Qy        236 ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
              ::  |||  |  |    |  :  |:    :|     :|| :||::|: :  :| :  ::
Db        268 MKTLNLRARLDF-QTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR 326

Qy        292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                | :  :|  :   : |||  :: |
Db        327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351


RESULT 3
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g103
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

  Query Match             19.6%;  Score 362.5;  DB 2;  Length 373;
  Best Local Similarity   27.5%;  Pred. No. 1.3e-25;
  Matches   92;  Conservative   68;  Mismatches  140;  Indels   35;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :|  |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::|   :|  :   :::   ::|         |: : |          | :
Db        174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |      :|:   :::|  ||   |:|       :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|     :|| :||::|: :  :| :  ::
Db        288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR--------- 337

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                  |  |  | : :      ::: : |:   |
Db        338 --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370


RESULT 4
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g18394
R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
```

```
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-deper

  Query Match             19.1%;  Score 354;  DB 2;  Length 373;
  Best Local Similarity   29.2%;  Pred. No. 8.2e-25;
  Matches   93;  Conservative   66;  Mismatches  132;  Indels   28;  Gaps    8;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |:::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :| |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::   :|  :   |::  ::|          |: : |          | :
Db        174 LVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |      :|:   :::|  ||   |:|       :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|      :|| :||::|: :  :| :   :|   : |
Db        288 LDF-QTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR---RLSRATRKAS 343

Qy        301 QPGHSKTQ-RPEEMPISNL 318
              :   :  | : |:| :: |
Db        344 RRSEANLQSKSEDMTLNIL 362


RESULT 5
JC5549
heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5549
R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2
C;Superfamily: ATP receptor P2u

  Query Match             18.5%;  Score 343.5;  DB 2;  Length 370;
  Best Local Similarity   31.0%;  Pred. No. 7.5e-24;
  Matches   94;  Conservative   52;  Mismatches  130;  Indels   27;  Gaps   10;

Qy         24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
              | |:|| : | |:|  ||| ||    : ::: ||||:| | :  |||:  :|   ||| |
Db         48 VVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPF 106

Qy         84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
              ||  |::       |  ||::||| :: ||:  :|:|  :  || ||  : |||  :| |
Db        107 GDTLCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRS-RTIRTRRNSAIVCAGVWIL 165

Qy        143 VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE-------FFMPLGIILFC 195
              |: | :   | :   |      :|  |   |   |   : ::          | :|| : : |
Db        166 VLSGGISASLFSTTNVNNATTTC--FEGLSKRVWKTYLSKITIFIEVVGFIIPLILNVSC 223

Qy        196 SFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC-- 252
              |  :: :||:   |::     ||  : | |   ||: |::|  |  : ||: :  |
Db        224 SSVVLRTLRKPATLSQIGTNKKKVLKMITVHMAVFVVCFVPYNS--VLFLYALVRSQAIT 281

Qy        253 ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSKT 307
                  :       |||    :|   || :|||:  || | ||    |     :     ||
Db        282 NCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKSFYINAHI-----RMESLFKT 336

Qy        308 QRP 310
              : |
Db        337 ETP 339


RESULT 6
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g30438
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

  Query Match             18.3%;  Score 339;  DB 2;  Length 308;
  Best Local Similarity   30.3%;  Pred. No. 1.6e-23;
  Matches   91;  Conservative   56;  Mismatches  123;  Indels   30;  Gaps   10;

Qy         24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
              : |||| : | ||:  | | :|    :| |: |||::| | :  ||||  ||   |:| |
Db         23 MVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLLFVFTLPFRI-YYFVVRNWPF 81

Qy         84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
              ||: |:: :     |  |||:||| :: ||:  :|||  :  |: |:  | |||  :|
Db         82 GDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRS-KTLRTKRNARIVCVAVWIT 140

Qy        143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL-------EFFMPLGII 192
              |: |:    :     |      |     |:|     : |   : ::         ||:|| :
Db        141 VLAGSTPASFFQSTNRQNNTEQRTCFENF---PESTWKTYLSRIVIFIEIVGFFIPLILN 197

Qy        193 LFCSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV 247
              : ||  :: :| :   |:| :   ||  : | |  ::|  |::| :::  || |     |
Db        198 VTCSTMVLRTLNKPLTLSRNKLSKKKVLKMIFVHLVIFCFCFVPYNITLILYSLMRTQTW 257

Qy        248 PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT 307
              : :   :|      :||      |   ||:||||:| :  :          |  ||  |  |
Db        258 INCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNSE---------LDKKQQVHQNT 308


RESULT 7
T09508
```

```
intron 17 purinergic receptor P2Y5 - human
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             17.5%;  Score 324;  DB 2;  Length 344;
  Best Local Similarity   30.8%;  Pred. No. 4.3e-22;
  Matches   88;  Conservative   56;  Mismatches  120;  Indels   22;  Gaps   10;

Qy         24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
              : |||| : | ||:  |   :|    :| |: |||::| | :  |||| :|   |:| |
Db         26 MVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDLLFVFTLPFRI-FYFTTRNWPF 84

Qy         84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
              ||: |:: :     |  |||:||| :: ||:  :|:|  :  |: |:  | |||| :|
Db         85 GDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFKS-KTLRTKRNAKIVCTGVWLT 143

Qy        143 VILGT--VYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL-------EFFMPLGIIL 193
              || |:     :   |      : :|     |:   |   : ::         ||:|| : :
Db        144 VIGGSAPAVFVQSTHSQGNNASEACFENFPEAT--WKTYLSRIVIFIEIVGFFIPLILNV 201

Qy        194 FCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARLYFL---WTVP 248
               ||  :: :| :   |:|     | |  : | |  |:|  |::| :::  || |     |
Db        202 TCSSMVLKTLTKPVTLSRSKINKTKVLKMIFVHLIIFCFCFVPYNINLILYSLVRTQTFV 261

Qy        249 SSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
              : :   :|     |||     |   ||:||||:| :     | :|:
Db        262 NCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFTSDT---IQNSIKM 304


RESULT 8
A47556
ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

  Query Match             17.3%;  Score 320;  DB 2;  Length 373;
  Best Local Similarity   30.1%;  Pred. No. 1.1e-21;
  Matches   98;  Conservative   44;  Mismatches  150;  Indels   34;  Gaps    8;

Qy          4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
              |  ||   |    ::|    |  |||   | |||  |   :|||  || |:|:|||:| |
Db         22 GYKCRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSL 81

Qy         64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                 ||   || |  || |  : |::  |    |  ||:||| ::  |   |: | |:
Db         82 YAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHS 141

Qy        124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCES---------FIMESAN 174
              :     | |  :   :| ||:     :|      |: | ::|           |:  |:
Db        142 LRWGRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSS- 200

Qy        175 GWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQQ--------LARQARMKKATRFIMVVA 226
                :| | | :|  :|| |    |   ||  :         | |  |  |: | | :|
Db        201 ----VMLGLLFAVPFSVILVC---YVLMARRLLKPAYGTTGGLPRAKR--KSVRTIALVL 251

Qy        227 IVFITCYLP-SVSARLYFLWTVPSSACDP--SVHGALHITLSFTYMNSMLDPLVYYFSSP 283
              ||  |:||  |:  ||: :     :|    ::: |  ||       || |||::|: :
Db        252 AVFALCFLPFHVTRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAGQ 311

Qy        284 SFPKFYNKLKICSLKPKQPGHSKTQR 309
              :|    |     | :|  |  |
Db        312 RLVRFARDAK----PPTEPTPSPQAR 333


RESULT 9
I51667
thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51667
R;Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C
Nature 368, 648-651, 1994
A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A;Reference number: I51667; MUID:94195429; PMID:8145852
A;Accession: I51667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-420 <GER>
A;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g4951

  Query Match             16.8%;  Score 310.5;  DB 2;  Length 420;
  Best Local Similarity   28.0%;  Pred. No. 9.3e-21;
  Matches   88;  Conservative   56;  Mismatches  133;  Indels   37;  Gaps   10;

Qy         14 ISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTD 73
              ::: :| |  | ||::|   | :|:  | | ||  ||: ||: |||:||   :  |||:
Db        100 LTKFVPSLYTVVFIVGLPLNLLAIIIFLFKMKVRKPAVVYMLNLAIADVFFVSVLPFKIA 159

Qy         74 YYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAA 133
              |:|    | ||   ||:       |   |:: :  :: ||:  ||:| |:::   |   |
Db        160 YHLSGNDWLFGPGMCRIVTAIFYCNMYCSVLLIASISVDRFLAVVYPMHSLSW-RTMSRA 218

Qy        134 GIVCT-LWALVILGTVYLLL--ENHLCVQETAVSCESFI-MESANGWHDIMFQ----LEF 185
              : |: :| : |  |: ||:  :     :    :|   : ::    ::   |     | |
Db        219 YMACSFIWLISIASTIPLLVTEQTQKIPRLDITTCHDVLDLKDLKDFYIYYFSSFCLLFF 278

Qy        186 FMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITC-----------YL 234
              |:|  |   |   |: ||     :    :  :|    :||  ||| |           ||
Db        279 FVPFIITTICYIGIIRSL-SSSSIENSCKKTRALFLAVVVLCVFIICFGPTNVLFLTHYL 337

Qy        235 PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
              :  ||| : :  |||  ||           :  ||||:||::|    ::   | :
Db        338 QEANEFLYFAYIL--SACVGSV-------------SCCLDPLIYYYASSQCQRYLYSL-L 381

Qy        295 CSLKPKQPGHSKTQ 308
              |  |  :|| |  |
Db        382 CCRKVSEPGSSTGQ 395


RESULT 10
I57940
somatostatin receptor 5 - rat
N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I57940; I57949; S39244
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
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A;Reference number: I57940; MUID:93125499; PMID:1362243
A;Accession: I57940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-363 <OCA1>
A;Cross-references: UNIPROT:P30938; GB:L04535; NID:g409238; PIDN:AAA17029.1; PID:g409239
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: I57949; MUID:94088493; PMID:8264565
A;Accession: I57949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 341-363 <OCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental source: pituitary
R;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat somatosta
A;Reference number: S39244
A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin

  Query Match             16.7%;  Score 309.5;  DB 2;  Length 363;
  Best Local Similarity   29.6%;  Pred. No. 9.8e-21;
  Matches   96;  Conservative   53;  Mismatches  148;  Indels   27;  Gaps    9;

Qy         17 VMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYL 76
              ::| | ::   :|  || : :    | |    : ||: |||||| | |: |||
Db         39 LVPVLYLLVCTVGLSGNTLVIYVVLRHAKMKTVTNVYILNLAVADVLFMLGLPFLATQNA 98

Qy         77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
                :| ||   ||: :    :|:  ||  | |:: ||| ||||  :       |||
Db         99 VVSYWPFGSFLCRLVMTLDGINQFTSIFCLMVMSVDRYLAVVHPLRSARWRRPRVAKMAS 158

Qy        137 CTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQ----LEFFMPLGII 192
              :|   :| :: ||:     |||   :|      |    |          | || || :|
Db        159 AAVWVFSLLMSLPLLV--FADVQEGWGTCNLSWPEPVGLWGAAFITYTSVLGFFGPLLVI 216

Qy        193 LFCSFKIVWSLR---RRQQLARQARMK-KATRFIMVVAIVFITCYLPSVSARLYFL-WTV 247
                |   ||  ::    |   :|: | : | || ::|| :||: |:||     :  | :|:
Db        217 CLCYLLIVVKVKAAGMRVGSSRRRRSEPKVTRMVVVVVLVFVGCWLPFFIVNIVNLAFTL 276

Qy        248 PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKIC--------SLKP 299
              |    :|:  |      :  :| ||  :||:| | | :| : : |: :|
Db        277 PE---EPTSAGLYFFVVVLSYANSCANPLLYGFLSDNFRQSFRKV-LCLRRGYGMEDADA 332

Qy        300 KQPGHSKTQRPEEMPISNLGRRSC 323
               :|   |: ||:    : |  |||
Db        333 IEPRPDKSGRPQ----ATLPTRSC 352


RESULT 11
C41795
somatostatin receptor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: C41795
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: UNIPROT:P30873; GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

  Query Match             16.6%;  Score 307;  DB 2;  Length 391;
  Best Local Similarity   25.7%;  Pred. No. 1.8e-20;
  Matches   85;  Conservative   62;  Mismatches  130;  Indels   54;  Gaps    9;

Qy          4 GSCCRIEGD----------------TISQVMPPLLIVAFV------LGALGNGVALCGF 40
              |:| | |                  |:|:     ::::|:      :|  || : :
Db         24 GACSRGPGSGAADGMEEPGRNASQNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVI 83

Qy         41 CFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRA 100
                : |    : :|: |||:|| |||: :||      |  ||| || : ||: |   |:|
Db         84 LRYAKMKTATNIYILNLAIADELLMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMF 142

Qy        101 GSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-Q 159
               ||  |||:: |||  |||| |        ||  :   :| | :|  : ::: :
Db        143 TSIYCLTVLSVDRYVAVVHPIKAARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANS 202

Qy        160 ETAVSCESFIMESANGWHD----IMFQLEFFMPLGIILFC-----------SFKIVWSLR 204
              :  |:|   : | |  |          | : | :|:| |  |               : |  |  |
Db        203 DGTVACNMLMPEPAQRWLVGFVLYTFLMGFLLPVGAICLCYVLIIAKMRMVALKAGWQQR 262

Qy        205 RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITL 264
              :| :       :| |  :|:| :||: |::|    :|  ::     |           :::
Db        263 KRSE-------RKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDAT------VSQLSV 309

Qy        265 SFTYMNSMLDPLVYYFSSPSFPKFYNKLKIC 295
                | ||  :|::| | | :| : : :: :|
Db        310 ILGYANSCANPILYGFLSDNFKRSFQRI-LC 339


RESULT 12
A41795
somatostatin receptor 1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: A41795
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: UNIPROT:P30872; GB:M81829; NID:g307433; PIDN:AAA58247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
C;Genetics:
A;Gene: GDB:SSTR1
A;Cross-references: GDB:134185; OMIM:182451
A;Map position: 14q13-14q13
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
F;58-84/Domain: transmembrane #status predicted <TM1>
F;95-120/Domain: transmembrane #status predicted <TM2>
F;132-153/Domain: transmembrane #status predicted <TM3>
F;173-195/Domain: transmembrane #status predicted <TM4>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;269-296/Domain: transmembrane #status predicted <TM6>
F;302-326/Domain: transmembrane #status predicted <TM7>
F;4,44,48,381/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;130-208/Disulfide bonds: #status predicted
F;172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic
F;265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;339/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             16.5%;  Score 305.5;  DB 2;  Length 391;
  Best Local Similarity   26.3%;  Pred. No. 2.5e-20;
  Matches   81;  Conservative   62;  Mismatches  128;  Indels   37;  Gaps    8;

Qy         10 EGDTISQVMPPLLIVAFV------LGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
              :  |:|:     ::::|:      :|  || : :     : |    : :|: |||:|| |
Db         47 QNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADEL 106
```

```
Qy          64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
               ||: :||      |  ||| || : ||: |   |:|   ||  |||:: |||  ||||  |
Db         107 LMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKA 165

Qy         124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-QETAVSCESFIMESANGWHD---- 178
                  ||  :   :| | :|  : ::: :      :  |:|   : | |  |
Db         166 ARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVL 225

Qy         179 IMFQLEFFMPLGIILFC-----------SFKIVWSLRRRQQLARQARMKKATRFIMVVAI 227
               | : | :|:| | |           : |  | |:| :       :| |  :|:| :
Db         226 YTFLMGFLLPVGAICLCYVLIIAKMRMVALKAGWQQRKRSE-------RKITLMVMMVVM 278

Qy         228 VFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK 287
               ||: |::|    :|  ::      |          :::  | ||  :|::| | | :| :
Db         279 VFVICWMPFYVVQLVNVFAEQDDAT------VSQLSVILGYANSCANPILYGFLSDNFKR 332

Qy         288 FYNKLKIC 295
                : :: :|
Db         333 SFQRI-LC 339
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RESULT 13
A39297
somatostatin receptor - rat
N;Alternate names: probable G-protein-coupled receptor; SRIF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C;Accession: A39297; A45102; S20088
R;Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expresse
A;Reference number: A39297; MUID:92096119; PMID:1661599
A;Accession: A39297
A;Molecule type: mRNA
A;Residues: 1-391 <MEY>
A;Cross-references: UNIPROT:P28646; GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; P
A;Experimental source: brain
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiat
R;Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A;Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A;Reference number: A45102; MUID:93016064; PMID:1400442
A;Accession: A45102
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-391 <LI1>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:116692)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

  Query Match   16.5%; Score 305.5; DB 2; Length 391;
  Best Local Similarity 26.3%; Pred. No. 2.5e-20;
  Matches   81; Conservative   62; Mismatches 128; Indels   37; Gaps   8;

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Qy          10 EGDTISQVMPPLLIVAFV------LGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
               :  |:|:     ::::|:      :|  || : :     : |    : :|: |||:|| |
Db          47 QNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADEL 106

Qy          64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
               ||: :||      |  ||| || : ||: |   |:|   ||  |||:: |||  ||||  |
Db         107 LMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMFTSIYCLTVLSVDRYVAVVHPIKA 165

Qy         124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-QETAVSCESFIMESANGWHD---- 178
                  ||  :   :| | :|  : ::: :      :  |:|   : | |  |
Db         166 ARYRRPTVAKVVNLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMPEPAQRWLVGFVL 225

Qy         179 IMFQLEFFMPLGIILFC-----------SFKIVWSLRRRQQLARQARMKKATRFIMVVAI 227
               | : | :|:| | |           : |  | |:| :       :| |  :|:| :
Db         226 YTFLMGFLLPVGAICLCYVLIIAKMRMVALKAGWQQRKRSE-------RKITLMVMMVVM 278

Qy         228 VFITCYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK 287
               ||: |::|    :|  ::      |          :::  | ||  :|::| | | :| :
Db         279 VFVICWMPFYVVQLVNVFAEQDDAT------VSQLSVILGYANSCANPILYGFLSDNFKR 332

Qy         288 FYNKLKIC 295
                : :: :|
Db         333 SFQRI-LC 339
```

RESULT 14
S15403
angiotensin II receptor type 1 - bovine
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S15403
R;Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiote
A;Reference number: S15403; MUID:91251900; PMID:2041569
A;Accession: S15403
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <SAS>
A;Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C;Superfamily: vertebrate rhodopsin

  Query Match   16.4%; Score 304.5; DB 2; Length 359;
  Best Local Similarity 24.9%; Pred. No. 2.8e-20;
  Matches   81; Conservative   68; Mismatches 143; Indels   33; Gaps   8;

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Qy          17 VMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYL 76
               ::| |  : ||:|  || : :    |:||    ::|:| |||:||   :: ||    |
Db          30 MIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYTA 89

Qy          77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
                    | ||:  |::   ::: |   |:  || :: |||  :|||  :     | : | :
Db          90 MEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKS-RLRRTMLVAKVT 148

Qy         137 C-TLWALVILGTVYLLL-ENHLCVQETAVSCESFIMESANGWHDIMFQLE-----FFMPL 189
               |  :| |  | ::  ::  |   :: | ::  :|  || |    :     |   |
Db         149 CIIIWLLAGLASLPTIIHRNVFFIENTNITVCAFHYESQNSTLPVGLGLTKNILGFLFPF 208

Qy         190 GIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIV--FITCYLP----SVSARLYF 243
                :|:  |: ::|   ::    :: : :|   | :::|||  |   ::|    :    |
Db         209 -LIILTSYTLIWKTLKKAYEIQKNKPRKDDIFKIILAIVLFFFFSWVPHQIFTFMDVLIQ 267

Qy         244 LWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFY-------------- 289
               |  :     :  |  |: ||:   | |: |:|| | |    | |::
Db         268 LGLIRDCKIEDIVDTAMPITICLAYFNNCLNPLFYGFLGKKFKKYFLQLLKYIPPKAKSH 327

Qy         290 ----NKLKICSLKPKQPGHSKTQRP 310
                   |:   | :| : |:| |::|
Db         328 SNLSTKMSTLSYRPSENGNSSTKKP 352
```

RESULT 15
B41795
somatostatin receptor 2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: B41795
A;Molecule type: DNA
A;Residues: 1-369 <YAM>
A;Cross-references: UNIPROT:P30874; GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A;Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C;Genetics:
A;Gene: GDB:SSTR2
A;Cross-references: GDB:134186; OMIM:182452
A;Map position: 17q24-17q24

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A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F;44-69/Domain: transmembrane #status predicted <TM1>
F;80-105/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;158-180/Domain: transmembrane #status predicted <TM4>
F;205-235/Domain: transmembrane #status predicted <TM5>
F;254-281/Domain: transmembrane #status predicted <TM6>
F;288-315/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32,351/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;115-193/Disulfide bonds: #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F;328/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             16.3%;  Score 302.5;  DB 2;  Length 369;
  Best Local Similarity   29.8%;  Pred. No. 4.4e-20;
  Matches   90;  Conservative   50;  Mismatches  135;  Indels   27;  Gaps    9;

Qy         13 TISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRT 72
              | : |:  :  |  ::|  || : :     : |    : :|: |||:|| | |: |||
Db         41 TSNAVLTFIYFVVCIIGLCGNTLVIYVILRYAKMKTITNIYILNLAIADELFMLGLPFLA 100

Qy         73 DYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVA 132
                :   || ||   ||| :    :|:  ||  |||:: |||  ||||  :       | |
Db        101 -MQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRRPRTA 159

Qy        133 AGIVCTLWA---LVILG-TVYLLLENHLCVQETAVSCESFIMESANGWHD----IMFQLE 184
              |   :|    ||||   :|  | ::   |    ||       :  |:       | |
Db        160 KMITMAVWGVSLLVILPIMIYAGLRSN---QWGRSSCTINWPGESGAWYTGFIIYTFILG 216

Qy        185 FFMPLGIILFCSFKIVWSLR----RRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              | :|| ||  |   |:  ::    |     |:   || || : :|  ||| |:||
Db        217 FLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLP----- 271

Qy        241 LYFLWTVPSSAC----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS 296
               :::: | | :      |:: |     :  || ||  :|::| | | :| | :  : :|
Db        272 -FYIFNVSSVSMAISPTPALKGMFDFVVVLTYANSCANPILYAFLSDNFKKSFQNV-LCL 329

Qy        297 LK 298
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Db        330 VK 331


Search completed: August 30, 2005, 18:34:36
Job time : 44 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:25:17 ; Search time 43 Seconds
(without alignments)
600.665 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	881.5	47.6	387	4	US-09-170-496D-222	Sequence 222, App
2	880.5	47.5	387	4	US-09-170-496D-108	Sequence 108, App
3	880.5	47.5	387	4	US-09-944-807-21	Sequence 21, Appl
4	529	28.5	423	2	US-08-955-713-2	Sequence 2, Appli
5	510	27.5	476	2	US-08-955-713-4	Sequence 4, Appli
6	451.5	24.4	319	3	US-09-130-749-2	Sequence 2, Appli
7	451.5	24.4	319	3	US-09-130-749-2	Sequence 2, Appli
8	448.5	24.2	319	4	US-09-170-496D-60	Sequence 60, Appl
9	448.5	24.2	319	4	US-09-170-496D-196	Sequence 196, App
10	371	20.0	362	3	US-08-513-974B-374	Sequence 374, App
11	362.5	19.6	373	2	US-08-559-524A-4	Sequence 4, Appli
12	362.5	19.6	373	3	US-08-749-707-4	Sequence 4, Appli
13	362.5	19.6	373	4	US-09-947-922-4	Sequence 4, Appli
14	361.5	19.5	346	4	US-09-585-876-2	Sequence 2, Appli
15	354	19.1	373	4	US-09-745-842-14	Sequence 14, Appl
16	346.5	18.7	370	3	US-08-781-250-2	Sequence 2, Appli
17	336	18.1	339	1	US-08-153-848-44	Sequence 44, Appl
18	336	18.1	339	2	US-08-812-871-3	Sequence 3, Appli
19	336	18.1	339	3	US-09-299-843A-44	Sequence 44, Appl
20	336	18.1	339	3	US-09-088-337B-44	Sequence 44, Appl
21	336	18.1	339	4	US-09-170-496D-32	Sequence 32, Appl
22	336	18.1	339	5	PCT-US93-11153-44	Sequence 44, Appl
23	336	18.1	339	5	PCT-US95-07180-2	Sequence 2, Appli
24	335	18.1	339	4	US-09-170-496D-182	Sequence 182, App
25	328.5	17.7	302	2	US-08-467-948A-30	Sequence 30, Appl
26	328.5	17.7	302	3	US-08-467-947A-30	Sequence 30, Appl
27	327	17.6	309	3	US-09-422-869-20	Sequence 20, Appl
28	325	17.5	344	2	US-08-467-948A-8	Sequence 8, Appli
29	325	17.5	344	3	US-08-467-947A-8	Sequence 8, Appli
30	315.5	17.0	374	4	US-09-102-710B-3	Sequence 3, Appli
31	314	16.9	373	3	US-08-513-974B-373	Sequence 373, App
32	308	16.6	325	1	US-08-118-270-51	Sequence 51, Appl
33	308	16.6	325	5	PCT-US93-08528-51	Sequence 51, Appl
34	307	16.6	391	1	US-07-816-283-4	Sequence 4, Appli
35	307	16.6	391	1	US-08-417-103-4	Sequence 4, Appli
36	307	16.6	395	1	US-08-097-938-5	Sequence 5, Appli
37	307	16.6	395	1	US-08-476-000-5	Sequence 5, Appli
38	307	16.6	395	1	US-08-472-840-5	Sequence 5, Appli
39	307	16.6	395	2	US-08-476-976-5	Sequence 5, Appli
40	307	16.6	395	3	US-08-474-410-5	Sequence 5, Appli
41	306	16.5	398	1	US-08-097-938-6	Sequence 6, Appli
42	306	16.5	398	1	US-08-476-000-6	Sequence 6, Appli
43	306	16.5	398	1	US-08-472-840-6	Sequence 6, Appli
44	306	16.5	398	2	US-08-476-976-6	Sequence 6, Appli
45	306	16.5	398	3	US-08-474-410-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-170-496D-222
; Sequence 222, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-222

Query Match 47.6%; Score 881.5; DB 4; Length 387;
Best Local Similarity 52.2%; Pred. No. 5e-68;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

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Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | |::|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:||  | |||||||: ||  |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :  |      |  | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :|||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAKTFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  |  ||||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              | |      |  : ::   ::      :  : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
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RESULT 2
US-09-170-496D-108
; Sequence 108, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-108

  Query Match             47.5%;  Score 880.5;  DB 4;  Length 387;
  Best Local Similarity   52.2%;  Pred. No. 6.1e-68;
  Matches  178;  Conservative   49;  Mismatches  107;  Indels    7;  Gaps    4;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | |::|:||:| : |: | ||||:||  ||||:|:|| | ::|||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:||  | |||||||: ||  |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :  |      |  | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :|||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  |  ||||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              | |      |  : ::    ::      :  : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355


RESULT 3
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. 6773895
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Method for identifying substances which positively
;  TITLE OF INVENTION:  influence inflammatory conditions of chronic
;  TITLE OF INVENTION:  inflammatory airway diseases
;  FILE REFERENCE: 082_00n
;  CURRENT APPLICATION NUMBER: US/09/944,807
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: UK 0021484.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-944-807-21

  Query Match             47.5%;  Score 880.5;  DB 4;  Length 387;
  Best Local Similarity   52.2%;  Pred. No. 6.1e-68;
  Matches  178;  Conservative   49;  Mismatches  107;  Indels    7;  Gaps    4;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | |::|:||:| : |: | ||||:||  ||||:|:|| | ::|||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:||  | |||||||: ||  |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :  |      |  | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :|||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  |  ||||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              | |      |  : ::    ::      :  : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355


RESULT 4
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
;  GENERAL INFORMATION:
;    APPLICANT:  SATHE, GANESH
;    APPLICANT:  MOONEY, JEFFREY
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  HALSEY, WENDY
;    TITLE OF INVENTION:  cDNA CLONE HEOAD54 THAT ENCODES        A HUMAN 7-TRANS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/955,713
;      FILING DATE:  23-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/050,124
;      FILING DATE:  18-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70087
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-955-713-2

Query Match 28.5%; Score 529; DB 2; Length 423;
Best Local Similarity 39.2%; Pred. No. 1.1e-37;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

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Qy          4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
              | |       :|  : |:| : |||| :|| :||  || | : |  :||:| :|  ||||
Db         81 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFL 140

Qy         64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
              |:  || | ||||    | ||   |:| || |: ||  |:|||| :| :|| ||| |||
Db        141 LISNLPLRVDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV 200

Qy        124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
              ::  |   || :  ||  :      |||  || :   :  || |: :     ::  ||
Db        201 LSRASVGAAARVAGGLWVGI------LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254

Qy        179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
               :: ||||:|| :|||    |  ::| |  |  ||  ::| | : :|  |:  |:|||:
Db        255 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 313

Qy        238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                 | :  |     :   |    ||    :|:|||:||:|||::| ||||:|
Db        314 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 362
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RESULT 5
US-08-955-713-4
; Sequence 4, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMA, DERK
; APPLICANT: HALSEY, WENDY
; TITLE OF INVENTION: cDNA CLONE HEOAD54 THAT ENCODES A HUMAN 7-TRANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-955-713-4

Query Match 27.5%; Score 510; DB 2; Length 476;
Best Local Similarity 39.6%; Pred. No. 5.4e-36;
Matches 110; Conservative 47; Mismatches 101; Indels 20; Gaps 6;

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Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              : |:| : |||| :|| :||  || | : |  :||:| :|  |||||:  || | ||||
Db          6 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 65

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                 | ||   |:| || |: ||  |:|||| :| :|| ||| ||| :|  |     | :
Db         66 HETWRFGAAACKVNLFMLSTNRKASVVFLTAIALNRYLKVVXPHHVLNRASVGAXARVXG 125

Qy        138 TLWALVILGTVYLLLENHLCVQETAVSCESFIM----ESANGWHDIMFQLEFFMPLGIIL 193
               :|  ::|    |||        :  || |: :     ::  ||  :: ||||:|| :||
Db        126 GIWVGILLLNGXLLLNTF-----SGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 180

Qy        194 FCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV---SARLYFLWTVPSS 250
               |    | ::| |  |  ||  ::| | : :|  |:  |:|||:    | :   |
Db        181 FAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWLSACR 239

Qy        251 A---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
              :   |    ||    :|:|||:||:|||::| ||||:|
Db        240 SLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 273
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RESULT 6
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031090
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; ELSHOURBAGY, NABIL
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-Aug-1998
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-130-749-2

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  Query Match           24.4%;  Score 451.5;  DB 3;  Length 319;
  Best Local Similarity  34.4%;  Pred. No. 3.8e-31;
  Matches  101;  Conservative   61;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |     | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||    |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |:| :| |:|:|||:  |: :|::| ::  :| ::::|   : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::   : |     :|     :| | ||::|:|:|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296


RESULT 7
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031344
;  GENERAL INFORMATION:
;    APPLICANT:  SHABON, USMAN
;    APPLICANT:  ELSHOURBAGY, NABIL
;    TITLE OF INVENTION:  MOLECULAR CLONING OF A 7TM
;    TITLE OF INVENTION:  RECEPTOR (GPR31A)
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/130,749
;      FILING DATE:  07-AUG-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GP-70513
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  319 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-130-749-2

  Query Match           24.4%;  Score 451.5;  DB 3;  Length 319;
  Best Local Similarity  34.4%;  Pred. No. 3.8e-31;
  Matches  101;  Conservative   61;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |     | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||    |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |:| :| |:|:|||:  |: :|::| ::  :| ::::|   : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::   : |     :|     :| | ||::|:|:|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296


RESULT 8
US-09-170-496D-60
; Sequence 60, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-60

  Query Match           24.2%;  Score 448.5;  DB 4;  Length 319;
  Best Local Similarity  34.0%;  Pred. No. 6.9e-31;
  Matches  100;  Conservative   62;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |     | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||    |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |:| :| |:|:|||:  |: :|::| ::  :| ::::|   : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::   : |     :|     :| | ||::|:|:|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRV 296


RESULT 9
US-09-170-496D-196
; Sequence 196, Application US/09170496D
; Patent No. 6555339
```

```
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-196

  Query Match             24.2%;  Score 448.5;  DB 4;  Length 319;
  Best Local Similarity   34.0%;  Pred. No. 6.9e-31;
  Matches  100;  Conservative   62;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |       ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |    | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||    |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
               |:| :| |:|:||:  |: :|::| ::  :| ::::|    : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAKALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::    : |     :|     :| | ||::|:::|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRV 296


RESULT 10
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  374:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  362 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-513-974B-374

  Query Match             20.0%;  Score 371;  DB 3;  Length 362;
  Best Local Similarity   29.1%;  Pred. No. 3.6e-24;
  Matches   95;  Conservative   60;  Mismatches  128;  Indels   44;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |: | ||| ||:  | |||: |   :||:||||:|||| :: ||    ||
Db         43 LPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYYFN 102

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||: |::  |   :|  |||:||| ::  ||  ||||  ::  :  : |  :
Db        103 KTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNAVYVSS 162

Qy        138 TLWALVILGTVYLLLENHL---------CVQETA----------VSCESFIMESANGWHD 178
               :||||:     :|  : :          |   ||            | :  |
Db        163 LVWALVVAVIAPILFYSGIGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM-------- 214

Qy        179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                    | :|  :|| |   || :|  :  |      :|:|  :::|  ||   |||
Db        215 ------FCIPFIVILGCYGLIVKALIYK-DLDNSPLRRKSTYLVIIVLTVFAVSYLPFHV 267

Qy        236 ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                  :: ||| |  |     | :  |:    :|     :|| :||::|: :  :| :  ::
Db        268 MKTLNLRARLDF-QTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR 326

Qy        292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
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Db        327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351


RESULT 11
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-559-524A-4

  Query Match             19.6%;  Score 362.5;  DB 2;  Length 373;
  Best Local Similarity   27.5%;  Pred. No. 2e-23;
  Matches   92;  Conservative   68;  Mismatches  140;  Indels   35;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :|  |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::|   :|  :  :::   ::|          |: : |            | :
Db        174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |      :|:   :::|  ||   |:|       :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|     :|| :||::|: :  :| :  ::
Db        288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR--------- 337

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                  |  |  |  : :      ::: : |:   |
Db        338 --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370


RESULT 12
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,707
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-01-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-707-4

  Query Match             19.6%;  Score 362.5;  DB 3;  Length 373;
  Best Local Similarity   27.5%;  Pred. No. 2e-23;
  Matches   92;  Conservative   68;  Mismatches  140;  Indels   35;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :|  |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::|   :|  :  :::   ::|          |: : |            | :
Db        174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |      :|:   :::|  ||   |:|       :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|     :|| :||::|: :  :| :  ::
Db        288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR--------- 337

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                  |  |  |  : :      ::: : |:   |
Db        338 --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370


RESULT 13
US-09-947-922-4
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; Sequence 4, Application US/09947922
; Patent No. 6680373
;  GENERAL INFORMATION:
;       APPLICANT: Conley, Pamela B.
;                  Jantzen, Hans-Michael
;       TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
;       NUMBER OF SEQUENCES: 14
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
;            STREET: 1800 M Street, N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20036-5869
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/947,922
;            FILING DATE: 07-Sep-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/749,707
;            FILING DATE: 15-NOV-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Adler, Reid G.
;            REGISTRATION NUMBER: 30,988
;            REFERENCE/DOCKET NUMBER: 044481-5010-01-US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-467-7000
;            TELEFAX: 202-467-7176
;  INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 373 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-922-4

  Query Match             19.6%;  Score 362.5;  DB 4;  Length 373;
  Best Local Similarity   27.5%;  Pred. No. 2e-23;
  Matches   92;  Conservative   68;  Mismatches  140;  Indels   35;  Gaps    7;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :|  |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::|   :|  :  :::   ::|           |: : |           | :
Db        174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |       :|:   :::|  ||   |:|        :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|     :|| :||::|: :  :| :  ::
Db        288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSR--------- 337

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
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Db        338 --ATRKASRRSEANLQSKSEDMTLNILSEFKQNGD 370


RESULT 14
US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria Alexandra
;  APPLICANT: Silos-Santiago, Immaculada
;  TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
;  TITLE OF INVENTION: Uses Thereof
;  FILE REFERENCE: 5800-88
;  CURRENT APPLICATION NUMBER: US/09/585,876
;  CURRENT FILING DATE: 2000-06-01
;  EARLIER APPLICATION NUMBER: 60/182,061
;  EARLIER FILING DATE: 2000-02-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-585-876-2

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  Best Local Similarity   29.9%;  Pred. No. 2.3e-23;
  Matches   94;  Conservative   67;  Mismatches  136;  Indels   17;  Gaps    8;

Qy          3 NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV 59
              |   | || :   :  | : :: |  | ||||::: |   :: :| ||   |:: |||:
Db         27 NSRNCTIE-NFKREFFPIVYLIIPFWGVLGNGLSIYVP---LQPYKKSTSVNVFMLNLAI 82

Qy         60 ADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH 119
              :| | :  |||| |||||   | |||: ||:  ::| :|   || ||||::  |:  :||
Db         83 SDLLFISTLPFRADYYLRGSSWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVH 142

Qy        120 PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
              |   ::  | | :| |:| :  ::|: :  :||::      :  ||     : :
Db        143 PFRLLHVTSIR-SAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTM 201

Qy        177 HDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCYL 234
              : |   :  :|  :  |   |:  | : :  :   :  :||   |::  |:|  |:|
Db        202 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 261

Qy        235 PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
              | : |   | |      |   :| || |||     |:  :||:|||:  :|    ::||
Db        262 PYHTLRTVHLTTWKVGLCKDRLHKALVITLVLAAAANACFNPLLYYFAGENFK---DRLK- 317

Qy        295 CSLKPKQPGHSKTQ 308
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Db        318 SALRKGHPQKAKTK 331


RESULT 15
US-09-745-842-14
; Sequence 14, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
;  APPLICANT:  Conley, Pamela B.
;  APPLICANT:  Jantzen, Hans-Michael
;  APPLICANT:  Ramakrishnan-DuBridge, Vanitha
;  APPLICANT:  Julius, David
;  APPLICANT:  Hollopeter, Gunter
;  APPLICANT:  COR Therapeutics, Inc.
;  TITLE OF INVENTION:  P2Y12 Receptor
;  FILE REFERENCE:  44481-5053-US
;  CURRENT APPLICATION NUMBER: US/09/745,842
;  CURRENT FILING DATE:  2000-12-26
;  PRIOR APPLICATION NUMBER:  US 60/171,622
;  PRIOR FILING DATE:  1999-12-23
;  NUMBER OF SEQ ID NOS:  21
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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;   FEATURE:
;   OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
US-09-745-842-14

  Query Match             19.1%;  Score 354;  DB 4;  Length 373;
  Best Local Similarity   29.2%;  Pred. No. 1.1e-22;
  Matches   93;  Conservative   66;  Mismatches  132;  Indels   28;  Gaps    8;

Qy         18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
              :| : |: |::| ||| ||:  | |||| |   :||:||||:|||| :: ||    ||
Db         54 LPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYYFN 113

Qy         78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
              :  | |||  |::  |   :|  |||:||| ::| ||  ||:|  ::  :  : |  |
Db        114 KTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICISV 173

Qy        138 TLWALVILGTVYLLLENHLCVQET-AVSC---------ESFIMESANGWHDIMFQLEFFM 187
               :| :|::    :|  :   |::   ::|          |: : |           | :
Db        174 LVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228

Qy        188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-------SVSAR 240
              || :|| |   || :|  :  |      :|:   :::|  ||   |:|       :: ||
Db        229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              | |  |    | :  |:    :|     :|| :||::|: :  :| :   :|   : |
Db        288 LDF-QTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR---RLSRATRKAS 343

Qy        301 QPGHSKTQ-RPEEMPISNL 318
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Db        344 RRSEANLQSKSEDMTLNIL 362


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Job time : 45 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:28:13 ; Search time 162 Seconds
(without alignments)
839.213 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1853	100.0	346	9	US-09-862-274-2	Sequence 2, Appli
2	1853	100.0	346	9	US-09-942-374-2	Sequence 2, Appli
3	1853	100.0	346	10	US-09-886-041-2	Sequence 2, Appli
4	1853	100.0	346	10	US-09-782-974C-80	Sequence 80, Appl
5	1853	100.0	346	14	US-10-188-149A-2	Sequence 2, Appli
6	1853	100.0	346	14	US-10-079-384-18	Sequence 18, Appl
7	1853	100.0	346	14	US-10-240-842-2	Sequence 2, Appli
8	1853	100.0	346	14	US-10-225-567A-668	Sequence 668, App
9	1853	100.0	346	14	US-10-201-481-7	Sequence 7, Appli
10	1853	100.0	346	14	US-10-278-141-3	Sequence 3, Appli
11	1853	100.0	346	14	US-10-321-807-24	Sequence 24, Appl
12	1853	100.0	346	14	US-10-076-260-2	Sequence 2, Appli
13	1853	100.0	346	14	US-10-044-643-2	Sequence 2, Appli
14	1853	100.0	346	15	US-10-296-081-3	Sequence 3, Appli
15	1853	100.0	346	15	US-10-210-172-178	Sequence 178, App
16	1853	100.0	346	15	US-10-210-172-184	Sequence 184, App
17	1853	100.0	346	15	US-10-210-172-188	Sequence 188, App
18	1853	100.0	346	15	US-10-343-650A-8	Sequence 8, Appli
19	1853	100.0	346	15	US-10-665-956-2	Sequence 2, Appli
20	1853	100.0	346	15	US-10-332-032-1	Sequence 1, Appli
21	1853	100.0	346	16	US-10-321-807-24	Sequence 24, Appl
22	1853	100.0	346	16	US-10-314-048A-24	Sequence 24, Appl
23	1853	100.0	346	16	US-10-482-151-6	Sequence 6, Appli
24	1853	100.0	346	17	US-10-897-815-24	Sequence 24, Appl
25	1853	100.0	346	17	US-10-635-398-78	Sequence 78, Appl
26	1853	100.0	346	17	US-10-635-398-82	Sequence 82, Appl
27	1853	100.0	346	17	US-10-635-398-90	Sequence 90, Appl
28	1853	100.0	346	17	US-10-467-492A-80	Sequence 80, Appl
29	1853	100.0	346	17	US-10-975-979-80	Sequence 80, Appl
30	1853	100.0	346	18	US-10-930-662-24	Sequence 24, Appl
31	1853	100.0	352	15	US-10-210-172-192	Sequence 192, App
32	1853	100.0	584	17	US-10-505-486-88	Sequence 88, Appl
33	1849	99.8	346	14	US-10-094-417-8	Sequence 8, Appli
34	1849	99.8	346	20	US-11-086-846-8	Sequence 8, Appli
35	1848	99.7	345	17	US-10-635-398-94	Sequence 94, Appl
36	1846	99.6	346	15	US-10-210-172-180	Sequence 180, App
37	1846	99.6	346	17	US-10-635-398-84	Sequence 84, Appl
38	1839	99.2	346	14	US-10-044-643-5	Sequence 5, Appli
39	1839	99.2	346	15	US-10-210-172-182	Sequence 182, App
40	1839	99.2	346	17	US-10-635-398-86	Sequence 86, Appl
41	1739	93.8	342	14	US-10-092-135-2	Sequence 2, Appli
42	1686	91.0	314	15	US-10-210-172-186	Sequence 186, App
43	1686	91.0	314	17	US-10-635-398-88	Sequence 88, Appl
44	1686	91.0	320	15	US-10-210-172-190	Sequence 190, App
45	1686	91.0	320	15	US-10-210-172-194	Sequence 194, App

ALIGNMENTS

RESULT 1
US-09-862-274-2
; Sequence 2, Application US/09862274
; Patent No. US20020052022A1
; GENERAL INFORMATION:
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: GATTU, MAHANANDEESHWAR
; APPLICANT: SHABON, USMAN
; APPLICANT: IGNAR, DIANE MICHELE
; TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE
; TITLE OF INVENTION: 7TMR (AXOR87)
; FILE REFERENCE: GP-70703-1
; CURRENT APPLICATION NUMBER: US/09/862,274
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 09/580,675
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: GB 0026839.1
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-862-274-2

Query Match 100.0%; Score 1853; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
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Db         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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Db         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 2
US-09-942-374-2
; Sequence 2, Application US/09942374
; Patent No. US20020137063A1
; GENERAL INFORMATION:
;  APPLICANT: Glucksmann, Maria Alexsandra
;  APPLICANT:  Gimeno, Ruth
;  APPLICANT:  White, David
;  TITLE OF INVENTION: 57242, a Human G-Protein Coupled
;  TITLE OF INVENTION:  Receptor Family Member and Uses Therefor
;  FILE REFERENCE: MPI2000-368P1R
;  CURRENT APPLICATION NUMBER: US/09/942,374
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: US 60/228,409
;  PRIOR FILING DATE: 2000-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: human
US-09-942-374-2

  Query Match             100.0%;  Score 1853;  DB 9;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Qy          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
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Db          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

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Db         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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Db         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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Db         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 3
US-09-886-041-2
; Sequence 2, Application US/09886041
; Publication No. US20030059869A1
; GENERAL INFORMATION:
;  APPLICANT: XIA, TAI-HE
;  APPLICANT:  NI, DONGHUI
;  APPLICANT:  EISHINGDRELO, HAIFENG
;  APPLICANT:  ARDATI, ALI
;  APPLICANT:  MINNICH, ANNE
;  APPLICANT:  JUPP, RAY
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
;  FILE REFERENCE: 41491
;  CURRENT APPLICATION NUMBER: US/09/886,041
;  CURRENT FILING DATE:  2001-06-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-041-2

  Query Match             100.0%;  Score 1853;  DB 10;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db           1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy         301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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RESULT 4
US-09-782-974C-80
; Sequence 80, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
;  APPLICANT: Vogeli, Gabriel
;  APPLICANT:  Lind, Peter
;  APPLICANT:  Wood, Linda S.
;  APPLICANT:  Parodi, Luis A.
;  TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
;  FILE REFERENCE: 411USPHRM311
;  CURRENT APPLICATION NUMBER: US/09/782,974C
;  CURRENT FILING DATE:  2002-09-04
;  PRIOR APPLICATION NUMBER: 60/165,838
;  PRIOR FILING DATE: 1999-11-16
;  PRIOR APPLICATION NUMBER: 09/714,449
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 60/198,568
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,071
;  PRIOR FILING DATE: 1999-11-17
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;  PRIOR APPLICATION NUMBER: 60/166,678
;  PRIOR FILING DATE: 1999-11-19
;  PRIOR APPLICATION NUMBER: 60/173,396
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/184,129
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/185,421
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/185,554
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: 60/186,530
;  PRIOR FILING DATE: 2000-03-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-782-974C-80

  Query Match             100.0%;  Score 1853;  DB 10;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
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Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
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Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
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Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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RESULT 5
US-10-188-149A-2
; Sequence 2, Application US/10188149A
; Publication No. US20030077734A1
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al.
;  TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
;  TITLE OF INVENTION:  RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL000782-CON
;  CURRENT APPLICATION NUMBER: US/10/188,149A
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: US 09/666,535
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US 60/230,459
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: US 60/192,419
;  PRIOR FILING DATE: 2000-03-27
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-188-149A-2

  Query Match             100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
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Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 6
US-10-079-384-18
; Sequence 18, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
;  APPLICANT: Communi, Didier
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 9409/2132
;  CURRENT APPLICATION NUMBER: US/10/079,384
;  CURRENT FILING DATE:  2002-02-20
;  PRIOR APPLICATION NUMBER: US 09/885,453
;  PRIOR FILING DATE: 2001-06-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-079-384-18

  Query Match             100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
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Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
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Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
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Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
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Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
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Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 7
US-10-240-842-2
; Sequence 2, Application US/10240842
; Publication No. US20030109673A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN-COUPLED RECEPTOR
;  FILE REFERENCE: 4974.00883
;  CURRENT APPLICATION NUMBER: US/10/240,842
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: 60/194,701
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-240-842-2

  Query Match            100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
                ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 8
US-10-225-567A-668
; Sequence 668, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 668
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-668

  Query Match            100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
                ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 9
US-10-201-481-7
; Sequence 7, Application US/10201481
; Publication No. US20030119024A1
; GENERAL INFORMATION:
;  APPLICANT: Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Biery, Matthew
;  TITLE OF INVENTION: Genes and Proteins Associated with T-Cell Activation
;  FILE REFERENCE: 9301-133-999
;  CURRENT APPLICATION NUMBER: US/10/201,481
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 60/306,968
;  PRIOR FILING DATE: 2001-07-20
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-201-481-7

  Query Match            100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
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Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 10
US-10-278-141-3
; Sequence 3, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
;  APPLICANT: PATTERSON, Chandra
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  LU, Yan
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  GRAUL, Richard
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  WALIA, Narinder K.
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  HAFALIA, April
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  REDDY, Roopa
;  APPLICANT:  KALLICK, Deborah A.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  AU-YOUNG, Janice
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0096 USA
;  CURRENT APPLICATION NUMBER: US/10/278,141
;  CURRENT FILING DATE:  2002-10-21
;  PRIOR APPLICATION NUMBER: 60/208,834
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/207,566
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: US01/16285
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: 60/205,628
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 60/208,861
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/206,222
;  PRIOR FILING DATE: 2000-05-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030138818A1 7474846CD1
US-10-278-141-3

  Query Match           100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 11
US-10-321-807-24
; Sequence 24, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Rupong
;  APPLICANT:  Dang, Huong T.
;  APPLICANT:  Lowitz, Kevin P.
;  TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN0086
;  CURRENT APPLICATION NUMBER: US/10/321,807
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: US/09/714,008
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: PCT/US99/23938
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/166,088
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,099
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/166,369
;  PRIOR FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 60/171,902
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,901
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/171,900
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/181,749
;  PRIOR FILING DATE: 2000-02-11
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-321-807-24

  Query Match           100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
```

```
Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 12
US-10-076-260-2
; Sequence 2, Application US/10076260
; Publication No. US20030171541A1
; GENERAL INFORMATION:
;  APPLICANT: Elliott, Steven G.
;  APPLICANT:  Rogers, No. US20030171541A1ma
;  APPLICANT:  Busse, Leigh Anne
;  TITLE OF INVENTION: G-Protein Coupled Receptor Molecules and Uses Thereof
;  FILE REFERENCE: 02-076
;  CURRENT APPLICATION NUMBER: US/10/076,260
;  CURRENT FILING DATE:  2002-02-14
;  PRIOR APPLICATION NUMBER: 60/269,040
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-076-260-2

  Query Match            100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 13
US-10-044-643-2
; Sequence 2, Application US/10044643
; Publication No. US20030195335A1
; GENERAL INFORMATION:
;  APPLICANT: Majumder, Kumud
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Mishnu, Vishun S
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Baumgartner, Jason C
;  APPLICANT:  Gusev, Vladimir
;  TITLE OF INVENTION: No. US20030195335A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 15966-748
;  CURRENT APPLICATION NUMBER: US/10/044,643
;  CURRENT FILING DATE:  2002-01-11
;  PRIOR APPLICATION NUMBER: 60/193,664
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 60/194,614
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 60/195,063
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,066
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,067
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,068
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,069
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,070
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,510
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/219,855
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 60/221,284
;  PRIOR FILING DATE: 2000-07-27
;  PRIOR APPLICATION NUMBER: 60/221,325
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/224,588
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/239,613
;  PRIOR FILING DATE: 2000-10-11
;  PRIOR APPLICATION NUMBER: 60/262,508
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: 60/263,604
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,433
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/265,161
;  PRIOR FILING DATE: 2001-01-30
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-044-643-2

  Query Match            100.0%;  Score 1853;  DB 14;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
```

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Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

RESULT 14
US-10-296-081-3
; Sequence 3, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 PCT
; CURRENT APPLICATION NUMBER: US/10/296,081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,861
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030220477A1 7474846CD1
US-10-296-081-3

Query Match 100.0%; Score 1853; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

RESULT 15
US-10-210-172-178
; Sequence 178, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOI
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16

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;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 327
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 178
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-210-172-178

  Query Match            100.0%;  Score 1853;  DB 15;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-163;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


Search completed: August 30, 2005, 18:38:12
Job time : 164 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:23:45 ; Search time 173 Seconds
(without alignments)
1024.158 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1853	100.0	346	1	GP81_HUMAN	Q9bxc0 homo sapien
2	1841	99.4	346	2	Q6NXU5	Q6nxu5 homo sapien
3	1483	80.0	343	1	GP81_MOUSE	Q8c131 mus musculu
4	883.5	47.7	363	2	Q8TDS4	Q8tds4 homo sapien
5	881.5	47.6	387	2	Q8NGE4	Q8nge4 homo sapien
6	880.5	47.5	387	1	G09B_HUMAN	P49019 homo sapien
7	868.5	46.9	360	2	Q9EP66	Q9ep66 mus musculu
8	862.5	46.5	360	2	Q80Z39	Q80z39 rattus norv
9	596	32.2	263	2	Q8NGV8	Q8ngv8 homo sapien
10	529	28.5	384	2	Q8NGW4	Q8ngw4 homo sapien
11	529	28.5	384	2	Q86WP7	Q86wp7 homo sapien
12	529	28.5	423	2	Q8TDS5	Q8tds5 homo sapien
13	450.5	24.3	319	2	Q9NQ20	Q9nq20 homo sapien
14	448.5	24.2	319	1	GP31_HUMAN	O00270 homo sapien
15	446.5	24.1	319	2	Q9JLS1	Q9jls1 mus musculu
16	375.5	20.3	309	2	Q8R528	Q8r528 mus musculu
17	371.5	20.0	309	1	CLT2_MOUSE	Q920a1 mus musculu
18	366.5	19.8	346	1	CLT2_HUMAN	Q9ns75 homo sapien
19	364	19.6	362	1	P2YR_CHICK	P34996 gallus gall
20	364	19.6	362	1	P2YR_MELGA	P49652 meleagris g
21	362.5	19.6	373	1	P2YR_BOVIN	P48042 bos taurus
22	362	19.5	345	1	CLT2_PIG	Q95n03 sus scrofa
23	358.5	19.3	373	1	P2YR_RAT	P49651 rattus norv
24	356.5	19.2	373	1	P2YR_CAVPO	P59902 cavia porce
25	355.5	19.2	309	1	CLT2_RAT	Q924t9 rattus norv
26	354	19.1	373	1	P2YR_HUMAN	P47900 homo sapien
27	351.5	19.0	373	1	P2YR_MOUSE	P49650 mus musculu
28	351.5	19.0	390	2	Q8QGQ4	Q8qgq4 carassius a
29	350.5	18.9	370	2	Q6NSP5	Q6nsp5 homo sapien
30	348.5	18.8	373	2	Q8BMJ5	Q8bmj5 mus musculu
31	346.5	18.7	370	1	P2Y9_HUMAN	Q99677 homo sapien
32	342.5	18.5	357	2	Q9DE05	Q9de05 raja erinac
33	341	18.4	361	2	Q90X57	Q90x57 xenopus lae
34	340.5	18.4	370	2	Q8BKK1	Q8bkk1 mus musculu
35	340	18.3	344	1	P2Y5_MOUSE	Q8bmc0 mus musculu
36	339	18.3	308	1	P2Y5_CHICK	P32250 gallus gall
37	337	18.2	339	2	Q8N5S7	Q8n5s7 homo sapien
38	336.5	18.2	370	2	Q8BLG2	Q8blg2 mus musculu
39	336	18.1	367	1	GP17_HUMAN	Q13304 homo sapien
40	336	18.1	390	2	Q8AXM7	Q8axm7 carassius a
41	333.5	18.0	339	2	Q6NS65	Q6ns65 mus musculu
42	330.5	17.8	383	2	Q6NV10	Q6nv10 brachydanio
43	330	17.8	347	2	Q7ZZA4	Q7zza4 brachydanio
44	329.5	17.8	380	2	Q9DGQ6	Q9dgq6 carassius a
45	327	17.6	309	1	GP35_HUMAN	Q9hc97 homo sapien

Nicotinic Niacin B3 AXOR 87 TGR 183 HGPRBMY29

ALIGNMENTS

RESULT 1
GP81_HUMAN
ID GP81_HUMAN STANDARD; PRT; 346 AA.
AC Q9BXC0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor (GPR81) (FKSG80 protein).
GN Name=GPR81; Synonyms=FKSG80;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Wang Y.-G., Gong L.;
RT "Molecular cloning of FKSG80, a novel gene encoding a putative
RT chemokine receptor.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in pituitary tissue. Not detected in
CC frontal, temporal and occipital lobes of the cortex, basal
CC forebrain, caudate nucleus, nucleus accumbens, and hippocampus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC ---

```
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AF411110; AAL26481.1; -.
DR   EMBL; AB083631; BAB89344.1; -.
DR   EMBL; AF345568; AAK29071.1; -.
DR   EMBL; AB065866; BAC06084.1; -.
DR   Genew; HGNC:4532; GPR81.
DR   MIM; 606923; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     21       Extracellular (Potential).
FT   TRANSMEM     22    42       1 (Potential).
FT   DOMAIN       43    49       Cytoplasmic (Potential).
FT   TRANSMEM     50    70       2 (Potential).
FT   DOMAIN       71    89       Extracellular (Potential).
FT   TRANSMEM     90    110      3 (Potential).
FT   DOMAIN       111   130      Cytoplasmic (Potential).
FT   TRANSMEM     131   151      4 (Potential).
FT   DOMAIN       152   182      Extracellular (Potential).
FT   TRANSMEM     183   203      5 (Potential).
FT   DOMAIN       204   220      Cytoplasmic (Potential).
FT   TRANSMEM     221   241      6 (Potential).
FT   DOMAIN       242   261      Extracellular (Potential).
FT   TRANSMEM     262   281      7 (Potential).
FT   DOMAIN       282   346      Cytoplasmic (Potential).
FT   DISULFID     88    165      By similarity.
FT   CARBOHYD     3     3        N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   346 AA;  39295 MW;  E0DB114EEB3A47A5 CRC64;

  Query Match             100.0%;  Score 1853;  DB 1;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-122;
  Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 2
Q6NXU5
ID   Q6NXU5       PRELIMINARY;      PRT;   346 AA.
AC   Q6NXU5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor 81.
GN   Name=GPR81;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC066883; AAH66883.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   346 AA;  39209 MW;  F916A8C273E53E63 CRC64;

  Query Match             99.4%;  Score 1841;  DB 2;  Length 346;
  Best Local Similarity   99.1%;  Pred. No. 1.2e-121;
  Matches  343;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              ||||||||||||||||||||||||||||||||||||||||||||:||| |||||||||||
Db         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADKYFKAVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKAARFIMVVAIVFITCYLPSVSAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346


RESULT 3
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```
GP81_MOUSE
ID   GP81_MOUSE     STANDARD;      PRT;   343 AA.
AC   Q8C131;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR81.
GN   Name=Gpr81;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AK029064; BAC26273.1; -.
DR   MGD; MGI:2441671; Gpr81.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN       1     21       Extracellular (Potential).
FT   TRANSMEM     22    42       1 (Potential).
FT   DOMAIN       43    49       Cytoplasmic (Potential).
FT   TRANSMEM     50    70       2 (Potential).
FT   DOMAIN       71    90       Extracellular (Potential).
FT   TRANSMEM     91    111      3 (Potential).
FT   DOMAIN       112   131      Cytoplasmic (Potential).
FT   TRANSMEM     132   152      4 (Potential).
FT   DOMAIN       153   182      Extracellular (Potential).
FT   TRANSMEM     183   203      5 (Potential).
FT   DOMAIN       204   220      Cytoplasmic (Potential).
FT   TRANSMEM     221   241      6 (Potential).
FT   DOMAIN       242   259      Extracellular (Potential).
FT   TRANSMEM     260   280      7 (Potential).
FT   DOMAIN       281   343      Cytoplasmic (Potential).
FT   DISULFID     88    165      By similarity.
FT   CARBOHYD     3     3        N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   343 AA;  38927 MW;  917FA9499B2E03FD CRC64;

  Query Match             80.0%;  Score 1483;  DB 1;  Length 343;
  Best Local Similarity   81.4%;  Pred. No. 1.8e-96;
  Matches  276;  Conservative   19;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
              | ||||| |||: |||||||||||: |||||||||:|||||||||||||| ||:||||||||
Db          1 MDNGSCCLIEGEPISQVMPPLLILVFVLGALGNGIALCGFCFHMKTWKSSTIYLFNLAVA 60

Qy         61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
              |||||||| |||||||||| |||| ||: || |||||||||||||||| |||||||||
Db         61 DFLLMICLPLRTDYYLRRRHWIFGDIACRLVLFKLAMNRAGSIVFLTVVAVDRYFKVVHP 120

Qy        121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
              || || || | ||   | || ||||||||||:|:||||| |  |||||||||||||:|
Db        121 HHMVNAISNRTAAATACVLWTLVILGTVYLLMESHLCVQGTLSSCESFIMESANGWHDVM 180

Qy        181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              ||||||:|| |||||  :|||||||| |||||::||||||| |||||||||| ||
Db        181 FQLEFFLPLTIILFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLAR 240

Qy        241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
              ||||||||:|||||||| |||:||||||:|||||||||||||| |||| || |||||||
Db        241 LYFLWTVPTSACDPSVHTALHVTLSFTYLNSMLDPLVYYFSSPSLPKFYTKLTICSLKPK 300

Qy        301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWD 339
              :|| :||:| |||||||| :| |  ||  |  ||||||
Db        301 RPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQWD 339


RESULT 4
Q8TDS4
ID   Q8TDS4      PRELIMINARY;      PRT;   363 AA.
AC   Q8TDS4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor HM74a (Seven transmembrane helix
DE   receptor).
GN   Name=GPCR;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA   Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA   Eilert M., Ignar D.M., Murdock P.R., Steplewski K., Green A.,
RA   Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA   Wilson S., Pike N.B.;
RT   "Molecular identification of high and low affinity receptors for
RT   nicotinic acid.";
RL   J. Biol. Chem. 278:9869-9874(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Elshourbagy N.A.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB083632; BAB89345.1; -.
DR   EMBL; AY148884; AAN71621.1; -.
DR   EMBL; AB065876; BAC06094.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   363 AA;  41849 MW;  C4B0EEC9CCB81D56 CRC64;

  Query Match             47.7%;  Score 883.5;  DB 2;  Length 363;
  Best Local Similarity   52.8%;  Pred. No. 2.5e-54;
  Matches  180;  Conservative   47;  Mismatches  107;  Indels    7;  Gaps    4;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | | :|:||:| : |: | ||||:||  ||||:|:|| | ::|||||||||||
Db         17 NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  | |:||  | |||||||: || ||||| |||:|||||| ||||:|||||||:
Db         77 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | || | || | | || : |  ||:|| :        |  | || :     ||: || ||
Db        137 NKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              ||:|||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        197 FFLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  |  |||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              |  |      |   : ::    ::      :  : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355


RESULT 5
Q8NGE4
ID   Q8NGE4      PRELIMINARY;      PRT;   387 AA.
AC   Q8NGE4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB065865; BAC06083.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   387 AA;  44495 MW;  26433C855E85EC81 CRC64;

  Query Match             47.6%;  Score 881.5;  DB 2;  Length 387;
  Best Local Similarity   52.2%;  Pred. No. 3.6e-54;
  Matches  178;  Conservative   49;  Mismatches  107;  Indels    7;  Gaps    4;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | |::|:||:| : |: | ||||:||  ||||:|:|| | ::|||||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:||  | |||||||: ||  |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :     |     | | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :|||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  |  |||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              |  |      |   : ::    ::      :  : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355


RESULT 6
G09B_HUMAN
ID   G09B_HUMAN     STANDARD;      PRT;   387 AA.
AC   P49019;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR109B (G protein-coupled
DE   receptor HM74).
GN   Name=GPR109B; Synonyms=HM74;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=94092629; PubMed=7505609;
RA   Nomura H., Nielsen B.W., Matsushima K.;
RT   "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT   leukocyte chemotactic peptide receptors.";
RL   Int. Immunol. 5:1239-1249(1993).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10923; BAA01721.1; -.
DR   PIR; I69202; I69202.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:16824; GPR109B.
DR   MIM; 606039; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN       1     28       Extracellular (Potential).
FT   TRANSMEM     29    50       1 (Potential).
FT   DOMAIN       51    63       Cytoplasmic (Potential).
FT   TRANSMEM     64    85       2 (Potential).
FT   DOMAIN       86    102      Extracellular (Potential).
FT   TRANSMEM     103   123      3 (Potential).
FT   DOMAIN       124   142      Cytoplasmic (Potential).
FT   TRANSMEM     143   163      4 (Potential).
FT   DOMAIN       164   194      Extracellular (Potential).
FT   TRANSMEM     195   209      5 (Potential).
FT   DOMAIN       210   236      Cytoplasmic (Potential).
FT   TRANSMEM     237   256      6 (Potential).
FT   DOMAIN       257   273      Extracellular (Potential).
FT   TRANSMEM     274   298      7 (Potential).
FT   DOMAIN       299   387      Cytoplasmic (Potential).
FT   DISULFID     100   177      By similarity.
SQ   SEQUENCE   387 AA;  44481 MW;  C244F562C2343647 CRC64;

  Query Match             47.5%;  Score 880.5;  DB 1;  Length 387;
  Best Local Similarity   52.2%;  Pred. No. 4.2e-54;
  Matches  178;  Conservative   49;  Mismatches  107;  Indels    7;  Gaps    4;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||     | |::|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db         17 NCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  |||:||  | |||||||: ||  |||| |||:|||||| ||||:|||||||:
Db         77 IICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | ||   || | | || : :  ||:|| :  |     |  | || :     ||: || ||
Db        137 NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE 196

Qy        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
              | :|||||||| :|:||||:| |: | |::|:|  |||||||| |:|||| |:
Db        197 FLLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255

Qy        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
              | : :|    |:   ||  | |||||||||||||:|||||||||| |:: |    |:
Db        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315

Qy        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
              | |     |   : ::    ::      : : |   | |
Db        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355


RESULT 7
Q9EP66
ID   Q9EP66      PRELIMINARY;      PRT;   360 AA.
AC   Q9EP66;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative seven transmembrane spanning receptor.
GN   Name=Gpr109b; Synonyms=Puma-g, Pumag;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ, and C57BL/6;
RA   Schaub A., Futterer A., Pfeffer K.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AJ300199; CAC17791.1; -.
DR   EMBL; AJ300198; CAC17790.1; -.
DR   MGD; MGI:1933383; Gpr109b.
DR   GO; GO:0016021; C:integral to membrane; IDA.
DR   GO; GO:0005525; F:GTP binding; IDA.
DR   GO; GO:0001614; F:purinergic nucleotide receptor activity; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   360 AA;  41400 MW;  CCCE52A2475777FC CRC64;

  Query Match             46.9%;  Score 868.5;  DB 2;  Length 360;
  Best Local Similarity   55.6%;  Pred. No. 2.8e-53;
  Matches  178;  Conservative   39;  Mismatches   96;  Indels    7;  Gaps    4;

Qy          3 NG-SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVAD 61
              || :||    : |::|:||:| :.|| | ||||:||  ||||:|:|| | ::||||||||
Db         11 NGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVAD 70

Qy         62 FLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPH 121
              |||:||||| || |:    | || ||||| || ||||| |||:|||||| ||||:|||||
Db         71 FLLIICLPFLTDNYVHNWDWRFGGIPCRVMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPH 130

Qy        122 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMF 181
              | :| || | || | | || | |  ||:||  | :     |  | || :     ||| ||
Db        131 HFLNKISNRTAAIISCFLWGLTIGLTVHLLYTNMMTKNGEAYLCSSFSICYNFRWHDAMF 190

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARL 241
              ||||:|| ||||||  :|:||||:| |: | |::|:|  |||||||||| |:||||: |:
Db        191 LLEFFLPLAIILFCSGRIIWSLRQR-QMDRHAKIKRAINFIMVVAIVFIICFLPSVAVRI 249

Qy        242 YFLWTVPS---SACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS 296
                | :       ||   ||  |   ||||||||||||:|||||||||| |::
Db        250 RIFWLLYKYNVRNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSFPNFFSTCINRC 309

Qy        297 LKPKQPGHSKTQRPEEMPIS 316
              |: |  |      |   : ::
Db        310 LRKKTLGEPDNNRSTSVELT 329


RESULT 8
Q80Z39
ID   Q80Z39      PRELIMINARY;      PRT;   360 AA.
AC   Q80Z39;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nicotinic acid receptor.
GN   Name=HM74b;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
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RA   Soga T., Kamhara M., Takasaki J., Matsumoto S., Saito T., Ohishi T.,
RA   Hiyama H., Matsuo A., Matsushime H., Furuichi K.;
RT   "Molecular identification of nicotinic acid receptor.";
RL   Biochem. Biophys. Res. Commun. 0:0-0(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB103062; BAC58009.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   360 AA;  41458 MW;  975BDEBCA448A6C5 CRC64;

  Query Match             46.5%;  Score 862.5;  DB 2;  Length 360;
  Best Local Similarity   54.7%;  Pred. No. 7.3e-53;
  Matches  175;  Conservative   43;  Mismatches   95;  Indels    7;  Gaps    4;

Qy          3 NG-SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVAD 61
              || :||    : |::|:||:| : || | ||||:||  ||||:|:|| | ::||||||||
Db         11 NGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVAD 70

Qy         62 FLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPH 121
              |||:||||| || |::   | || ||||| || ||||| |||:|||||| ||||:|||||
Db         71 FLLIICLPFLTDNYVQNWDWRFGSIPCRVMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPH 130

Qy        122 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMF 181
              | :| || | || | | || : |  ||:||  : :     |  | || :     ||| ||
Db        131 HFLNKISNRTAAIISCFLWGITIGLTVHLLYTDMMTRNGDANLCSSFSICYTFRWHDAMF 190

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARL 241
              ||||:|||||||||| :|:||||:| |: |  ::|:|  |||||||||: |:||||: |:
Db        191 LLEFFLPLGIILFCSGRIIWSLRQR-QMDRHVKIKRAINFIMVVAIVFVICFLPSVAVRI 249

Qy        242 YFLWTVPS---SACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS 296
                  | :       ||   ||  |   ||||||||||||:||||||||| |::
Db        250 RIFWLLYKHNVRNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSFPNFFSTCINRC 309

Qy        297 LKPKQPGHSKTQRPEEMPIS 316
              |: |  |     |   : ::
Db        310 LRRKTLGEPDNNRRSTSVELT 329


RESULT 9
Q8NGV8
ID   Q8NGV8      PRELIMINARY;      PRT;   263 AA.
AC   Q8NGV8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB065665; BAC05891.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   263 AA;  30289 MW;  F96BF023A5E1F1C1 CRC64;

  Query Match             32.2%;  Score 596;  DB 2;  Length 263;
  Best Local Similarity   59.9%;  Pred. No. 3e-34;
  Matches  115;  Conservative   23;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
              :||    | | :|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db         17 NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76

Qy         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
              :|||||  | |:||  | |||||||: || ||||| |||:|||||| ||||:|||||||:
Db         77 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136

Qy        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
              | || | || | | || : |  ||:|| :     |  | || :     ||: || ||
Db        137 NKISNRTAAIISCLLWGITIGLTVHLLKKKMPIPDGGANLCSSFSICHTLQWHEAMFLLE 196

Qy        185 FFMPLGIILFCS 196
              ||:|||||||||
Db        197 FFLPLGIILFCS 208


RESULT 10
Q8NGW4
ID   Q8NGW4      PRELIMINARY;      PRT;   384 AA.
AC   Q8NGW4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB065652; BAC05878.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; ISS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   384 AA;  41426 MW;  1C8455FED8085F36 CRC64;

  Query Match             28.5%;  Score 529;  DB 2;  Length 384;
  Best Local Similarity   39.2%;  Pred. No. 2.1e-29;
  Matches  115;  Conservative   48;  Mismatches  108;  Indels   22;  Gaps    7;

Qy          4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
              | |       :|  : |:| : |||| :|| :||  || | : |  :||:| :|  ||||
Db         42 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFL 101
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Qy          64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
               |:  || | ||||    | ||   |:| || |: ||  |:|||| :| :|| ||| |||
Db         102 LISNLPLRVDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV 161

Qy         124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
               ::  |   || :  ||  :      ||| || :   :  || |: :     ::  ||
Db         162 LSRASVGAAARVAGGLWVGI------LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 215

Qy         179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
               :: ||||:|| :|||    |  ::| |  |  ||  ::| | : :|  |:  |:|||:
Db         216 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 274

Qy         238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                 | :   |     :   |    ||    :|:|||:||:|||::| ||||:|
Db         275 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 323


RESULT 11
Q86WP7
ID   Q86WP7      PRELIMINARY;      PRT;   384 AA.
AC   Q86WP7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative 5-oxo-ETE G-protein coupled receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22495202; PubMed=12606753;
RA   Jones C.E., Holden S., Tenaillon L., Bhatia U., Seuwen K., Tranter P.,
RA   Turner J., Kettle R., Bouhelal R., Charlton S., Nirmala N., Jarai G.,
RA   Finan P.;
RT   "Expression and characterization of a 5-oxo-6E,8Z,11Z,14Z-
RT   eicosatetraenoic acid receptor highly expressed on human eosinophils
RT   and neutrophils.";
RL   Mol. Pharmacol. 63:471-477(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY158687; AAO17739.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; ISS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   384 AA;  41412 MW;  0C5E35FED8085F36 CRC64;

  Query Match             28.5%;  Score 529;  DB 2;  Length 384;
  Best Local Similarity   39.2%;  Pred. No. 2.1e-29;
  Matches  115;  Conservative   48;  Mismatches  108;  Indels   22;  Gaps    7;

Qy           4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
               | |       :|  : |:| : |||| :|| :||  || | : |  :||:| :|  ||||
Db          42 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFL 101

Qy          64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
               |:  || | ||||    | ||   |:| || |: ||  |:|||| :| :|| ||| |||
Db         102 LISNLPLRVDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV 161

Qy         124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
               ::  |   || :  ||  :      ||| || :   :  || |: :     ::  ||
Db         162 LSRASVGAAARVAGGLWVGI------LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 215

Qy         179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
               :: ||||:|| :|||    |  ::| |  |  ||  ::| | : :|  |:  |:|||:
Db         216 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 274

Qy         238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                 | :   |     :   |    ||    :|:|||:||:|||::| ||||:|
Db         275 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 323


RESULT 12
Q8TDS5
ID   Q8TDS5      PRELIMINARY;      PRT;   423 AA.
AC   Q8TDS5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   G-protein coupled receptor TG1019.
GN   Name=GPCR; Synonyms=OXER1, tg1019;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22191290; PubMed=12065583; DOI=10.1074/jbc.M203194200;
RA   Hosoi T., Koguchi Y., Sugikawa E., Chikada A., Ogawa K., Tsuda N.,
RA   Suto N., Tsunoda S., Taniguchi T., Ohnuki T.;
RT   "Identification of a Novel Human Eicosanoid Receptor Coupled to
RT   Gi/o.";
RL   J. Biol. Chem. 277:31459-31465(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB083630; BAB89343.1; -.
DR   EMBL; AB083055; BAC11806.2; -.
DR   EMBL; BC063549; AAH63549.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; NAS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; NAS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; NAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; IDA.
```

```
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   423 AA;  45810 MW;  72ADA9F43A9EC051 CRC64;

  Query Match             28.5%;  Score 529;  DB 2;  Length 423;
  Best Local Similarity   39.2%;  Pred. No. 2.3e-29;
  Matches  115;  Conservative   48;  Mismatches  108;  Indels   22;  Gaps    7;

Qy          4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGPCFHMKTWKPSTVYLFNLAVADFL 63
              | |       :|  : |:| : |||| :|| :||  || | : |  :||:| :|  ||||
Db         81 GPCHPTSSSLVSAFLAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFL 140

Qy         64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
              |:  || | ||||    | ||   |:| || |: ||  |:|||| :| :|| ||| |||
Db        141 LISNLPLRVDYYLLHETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHV 200

Qy        124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
              ::  |   || :  ||  :      |||  || :   :  || |: :     ::  ||
Db        201 LSRASVGAAARVAGGLWVGI------LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254

Qy        179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
              :: ||||:|| :|||    |  ::| |  |  ||  ::| | : :|  |: :|:|||:
Db        255 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 313

Qy        238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                | :   |    :   |   ||    :|:|||:||:|||:| ||||:|
Db        314 FGMASMVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 362


RESULT 13
Q9NQ20
ID   Q9NQ20      PRELIMINARY;      PRT;   319 AA.
AC   Q9NQ20;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BA517H2.2 (G protein-coupled receptor 31).
GN   Name=GPR31;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Almeida J.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL121935; CAB99329.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35074 MW;  2ACD0350AD7FB53A CRC64;

  Query Match             24.3%;  Score 450.5;  DB 2;  Length 319;
  Best Local Similarity   34.4%;  Pred. No. 5.9e-24;
  Matches  101;  Conservative   61;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGPCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |    | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALHFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||     |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |:| :| |:|:||:  |: :|::| ::  :| ::::|   : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::    : |    :|     :| | ||::|:|:|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296


RESULT 14
GP31_HUMAN
ID   GP31_HUMAN     STANDARD;      PRT;   319 AA.
AC   O00270;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR31.
GN   Name=GPR31;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97349123; PubMed=9205127; DOI=10.1006/geno.1997.4754;
RA   Zingoni A., Rocchi M., Storlazzi C.T., Bernardini G., Santoni A.,
RA   Napolitano M.;
RT   "Isolation and chromosomal localization of GPR31, a human gene
RT   encoding a putative G protein-coupled receptor.";
RL   Genomics 42:519-523(1997).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U65402; AAC51375.1; -.
DR   Genew; HGNC:4486; GPR31.
DR   MIM; 602043; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     16       Extracellular (Potential).
FT   TRANSMEM     17     37       1 (Potential).
FT   DOMAIN       38     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       2 (Potential).
FT   DOMAIN       74     91       Extracellular (Potential).
FT   TRANSMEM     92    110       3 (Potential).
FT   DOMAIN      111    131       Cytoplasmic (Potential).
FT   TRANSMEM    132    152       4 (Potential).
FT   DOMAIN      153    180       Extracellular (Potential).
FT   TRANSMEM    181    201       5 (Potential).
FT   DOMAIN      202    219       Cytoplasmic (Potential).
FT   TRANSMEM    220    240       6 (Potential).
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FT   DOMAIN      241    265       Extracellular (Potential).
FT   TRANSMEM    266    284       7 (Potential).
FT   DOMAIN      285    319       Cytoplasmic (Potential).
FT   CARBOHYD      5      5       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   319 AA;  35079 MW;  7A4F164CD9C969DD CRC64;

  Query Match             24.2%;  Score 448.5;  DB 1;  Length 319;
  Best Local Similarity   34.0%;  Pred. No. 8.1e-24;
  Matches  100;  Conservative   62;  Mismatches  121;  Indels   11;  Gaps    5;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      ::  :  || :   || ||| |||  | | :: |||  ||| |||:|| ||
Db          6 CSAPSTVVATAVGVLLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              ||||   :||  : |  | : |     | | ::|:  : ||  || ||| :||||   ||
Db         66 CLPFLAAFYLSLQAWHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
              :| : | |:   :| |::  |   || :     : :  | ||     |:|     | : :
Db        126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
               |:| :| |:|:||:  |: :|::| ::  :| ::::|   : :| ::|  |:||   ||
Db        183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                ::    : |     :|     :| | ||::|:::|:|| ||||:|   | ::
Db        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRV 296


RESULT 15
Q9JLS1
ID   Q9JLS1      PRELIMINARY;      PRT;   319 AA.
AC   Q9JLS1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   G protein coupled receptor.
GN   Name=Tcp10c;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99431663; PubMed=10501965;
RA   Schimenti J.C.;
RT   "ORFless, intronless, and mutant transcription units in the mouse t
RT   complex responder (Tcr) locus.";
RL   Mamm. Genome 10:969-976(1999).
DR   EMBL; AF140708; AAF26668.1; -.
DR   MGD; MGI:98543; Tcp10c.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35551 MW;  571F6DFB485BD7C4 CRC64;

  Query Match             24.1%;  Score 446.5;  DB 2;  Length 319;
  Best Local Similarity   32.5%;  Pred. No. 1.1e-23;
  Matches  104;  Conservative   64;  Mismatches  133;  Indels   19;  Gaps    7;

Qy          7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
              |      :   :  :| :  ||| :|| |||  | : :| |||  ||||||| ||| ||
Db          6 CSAASTVVETAVGTMLTLECVLGLMGNAVALWTFFYRLKVWKPYAVYLFNLVVADLLLAT 65

Qy         67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
              :||   :||: : |  | :||:: || || :    : ||  || |||  ||||   ||
Db         66 SVPFFAAFYLKGKTWKLGHMPCQLLLFLLAFSCGVGVAFLMTVALDRYLHVVHPRLRVNL 125

Qy        127 ISTRVAAGIVCTLWALVILGTVYLLLENHLC-VQETAVSCESFI----MESANGWHDIMF 181
              :| | | ||   :| |::: |   ||    |   : :  | ||       ::     :::|
Db        126 LSLRAAWGISSLIWLLMVVLTPQNLL---TCRTTQNSTECPSFYPTGGTKAIATCQEVLF 182

Qy        182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
              |:  :| |:| ||:  :: :|::|  :  :|  :::|   : :: ::|  |:|||| |
Db        183 FLQVLLPFGLISFCNSGLIRTLQKRLSESDKQPTIRRARVLVAIMLLLFGLCFLPSVLTR 242

Qy        241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                ::      | :   ::  |  |  | | ::| | | :| ||:|:|   | |: : ||:
Db        243 VLVHIFQEFKSCSVQQAIMRASDIAGSLTCLHSTLSPAIYCFSNPAFTHSYRKV-LKSLR 301

Qy        299 PKQPGHSKTQRPEEMPISNL 318
              :       ::  | |  ||
Db        302 GR-------RKAAESPSDNL 314


Search completed: August 30, 2005, 18:33:48
Job time : 175 secs
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